

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 28, 2005, 05:52:45 ; Search time 44 Seconds
(without alignments)
1187.402 Million cell updates/sec

Title: US-10-786-149-2

Perfect score: 2842

Sequence: 1 MLRSKRALPPPLMLLLGP.....LPAGSPFVIRNAKVAACI 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	897.5	31.6	480	2 UC7506	heparanase protein
2	416	14.6	521	2 T45608	hypothetical prote
3	169.5	6.0	190	2 T01953	hypothetical prote
4	112.5	4.0	356	2 F64383	hypothetical prote
5	111.5	3.9	575	2 T12094	beta-fructofuranos
6	111	3.9	670	2 T10666	hypothetical prote
7	111	3.9	688	2 S32961	hypothetical prote
8	111	3.9	2298	2 T49648	hypothetical prote
9	109.5	3.9	879	2 E91031	probable outer mem
10	108.5	3.8	411	2 S74760	hypothetical prote
11	107.5	3.8	500	2 D87541	beta-xylosidase (i
12	106	3.7	879	2 F85875	probable fibrinall
13	105	3.7	670	2 T38446	microtubule-associ
14	104.5	3.7	788	1 S00652	phosphoribosylamin
15	104	3.7	432	2 F70411	adenylosuccinate s
16	104	3.7	2013	2 A11489	probable peptidogl
17	103.5	3.6	587	2 S36231	beta-fructofuranos
18	103.5	3.6	676	2 AF1153	transcription anti
19	103.5	3.6	687	2 F65188	retrotransposon li
20	103	3.6	796	2 D97065	transketolase (amp
21	101	3.6	594	2 A82913	hypothetical prote
22	101	3.6	644	2 A97268	methionyl-tRNA syn
23	100.5	3.5	805	2 H72098	DNA gyrase, chain
24	100.5	3.5	805	2 C86525	DNA gyrase subunit
25	100.5	3.5	989	2 AE2140	toxin secretion AB
26	99.5	3.5	510	2 H69893	conserved hypochet
27	99.5	3.5	837	1 A31842	endo-1,4-beta-xyla
28	99	3.5	897	2 G02529	dynein heavy chain
29	99	3.5	4644	1 A38905	dynein heavy chain

30	98.5	3.5	596	2 T04506	hypothetical prote
31	98.5	3.5	629	2 C64180	hypothetical prote
32	98.5	3.5	654	2 T14202	NADH dehydrogenas
33	98.5	3.5	699	2 P65146	DNA topoisomerase
34	98.5	3.5	701	2 D98014	DNA topoisomerase
35	98.5	3.5	746	2 T46821	steroid hormone rece
36	98.5	3.5	746	2 A95420	Rhizobactin r
37	98.5	3.5	1012	2 JC5925	membrane K10cho pr
38	98	3.4	465	2 T19113	hypothetical prote
39	98	3.4	716	1 C60008	RNA-directed RNA p
40	98	3.4	760	1 T34414	hypothetical prote
41	98	3.4	817	2 H75035	probable membrane
42	97.5	3.4	454	2 T20829	probable serine ca
43	97.5	3.4	511	2 S61166	probable membrane
44	97.5	3.4	604	2 E75119	hypothetical prote
45	97.5	3.4	804	2 G71546	probable DNA gyrase

ALIGNMENTS

RESULT 1					
UC7506					
heparanase protein 2a - human					
C:Species: Homo sapiens (man)					
C>Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004					
C:Accession: UC7506					
R:McKenzie, E.; Tyson, K.; Stamps, A.; Smith, P.; Turner, P.; Barry, R.; Hircock, M.; Pa					
Biochem. Biophys. Res. Commun. 276, 1170-1177, 2000					
A>Title: Cloning and expression profiling of Hpa2, a novel mammalian heparanase family m					
A:Reference number: UC7506					
A:Accession: UC7506					
A:Molecule type: mRNA					
A:Residues: 1-480 <MCK>					
A:Cross-references: UNIPROT:Q9HB39; GB:A282885					
C:Comment: This protein, a intracellular membrane-bound enzyme, has biological and chera					
therapies.					
C:Gene(s):					
A:Gene: hpa2a					
A:Map position: 10q23-10q24					
C:Keywords: heparin binding; membrane bound					
Query Match					
Best Local Similarity 31.6%; Score 897.5; DB 2; Length 480;					
Matches 202; Conservative 74; Mismatches 146; Indels 139; Gaps 9;					
QY	20	PLGPLSPGAL-----PRPA-----QAQDVVDLDFGTQEPHLVSPS	55		
DB	18	PPACIAPGALVIALLLHLSSQAGDRRLPVDRRAAGLKEKTLILDVSTKPVATVNN	77		
QY	56	FLSVTIIDANLATDRFLLLSGPKLRTIARGLSPAYLRFSGTKTDFLIF----	DPKKEST	111	
DB	78	FLSLQDPSIIHD-GWLDPLSSKRLVTLARGLSPAYLRFSGTKTDFLQFQMLRNPAKR-	135		
QY	112	FEERSYWGQYNODICKYIIPDVEEKLRLFWPQEQDLLREHYOKKFKSTYSRSSVD	171		
DB	136	-----GGRCPP-----YLLKNYE-----	148		
QY	172	VLYTFANCGLDLIFGLNALRLTADLQWSSNAQLLDYSSKGVNISWELGNEPNSFLK	231		
DB	149	-----DEPNNTYT	156		
QY	222	KADIFINSQGGEDYIOHLKLR-STPKNAKLVDGVORRRKTAKLKSLFKAGGEVI	290		
DB	157	MKGRAVNSQJGKYIQLKSLLOPRTIYRSASLVGPNIGRRKNVIALLDGPMKAGSTV	216		
QY	291	DSVTNHYLYNGRATREDPLNPVLDIFISSVQKVFQVVESTRPGKKVMIGETSSAYCG	350		
DB	217	DAVTWQHCYIDGRVYKWDPLKTRLLDLSNQIKIQGVNVTYTPGKKIMLEGVTTISAG	276		
QY	351	GAPLLSDTFAAGFMWLDKLGLSARMGIEVVRQVFPFAGNHYLVDFNPDPYLSLIF	410		
DB	277	GTNNLSDSYAGFLMLNTLGMLANQGLDGVIRHSFFDHGYNHLVDQNFNPDPYLSLIF	336		

QY 411 KKLVTGVTMAVSQGSRR-----KLRYLHCTGTDNPRYEGDLTYXANTLNAVY 461
 Db 337 KRLGPGKVLVAHVAHQKRPGRVIRDLKRIYAACTNNHNNYRGSITLFIINLRSR 396
 QY 462 KYLRLPYEPENKQVDKYLRLGPHGLSKSVQNLGTLKVVNDQTLPLMEKRLRPSS 521
 Db 397 KKKIKLGLTRDKLVHGYLLQPYGQEGLSKSVQNLGQPLVAVDQTLPELKPRFLRGR 456
 QY 522 LGLPAFSYSPFVIRNAKVAAC 542
 Db 457 LVIPFVTMGFFVKKVNNALAC 477

RESULT 2

mp:Arachidonic acid synthase F13G24.30 - Arabidopsis thaliana
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
 R:Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Ba
 submitted to the Protein Sequence Database, December 1999
 A:Reference number: 223009
 A:Accession: T45608
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-521 <BEV>
 A:Cross-references: UNIPROT:O9SDA1; EMBL:AL133421
 A:Experimental source: cultivar Columbia; BAC clone F13G24
 C:Genetics:
 A:Map position: 5
 A:introns: 53/3; 66/1; 127/2; 177/1; 256/1; 319/2; 361/2; 394/3
 ;Note: F13G24.30

Query Match	14.6%	Score 416;	DB 2;	Length 521;
Best Local Similarity	29.2%;	Pred. No. 5.8e-23;		
Matches 154; Conservative	68;	Mismatch		

[illegible]

QY 135 DVEKRLLEMPYOELLREHYQKKFKNS--TYSRSSV-----DVLTYFANGSGDLITF 186
| : | : | : | : | : | :
db 95 -----pevym-----

QY	187	GINALLRTADIO-----MNSNAQLLDYCKSKGYNI-SWEIGNEPNSFLKADIFIN	238
Qb	133	GINNI pnnny pnnny pnnny pnnny pnnny pnnny pnnny pnnny pnnny pnnny	

[illegible]

294 TWHHYLYNGRT--ATREDPLNDVLDIFISSVKVF-----QVVESTRPGKKVWLGETBSA 347

348 YGGAPLSTPFAAGFMILDKLGLSARMGLVVMRQVFPGAQNYHLYDE - NEDPLDYWL 406

[illegible]

465 -----GRAGVTLLINLSNQSDFTVS 413
| RLPYPES---NKQVDKYLRR---LGPHG---ILISKVOL 495

496 NGITLKWDQUTPLMEKPLRP-GSSJGLPAPSYSPFVIRNAKVAAC 542

3 13 NQNSLNFIATIGDIPSL-EPVLRSVNSPLNVLPLSMSFIVLPNFEDASAC 520

RESULT 3
T01953
hypothetical protein T2L5.6 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999
C:Accession: T01953
#text_change 09-Jul-2004

RESULT 3

hypothetical protein TZL5.6 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01953
R:Gietzel, C.; Smith, A.; Le, T.
submitted to the EMBL Data Library, October 1998
A:Description: The sequence of A. thaliana TZL5.
A:Reference number: Z14470
A:Accession: T01953
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-190 <GRI>
A:Cross-references: UNIPROT:O82604; EMBL:AF096371; NID:G3695386; PID:G3695392
C:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Introns: 36/2; 69/3
A:Note: TZL5.6
C:Superfamily: *Arabidopsis thaliana* hypothetical protein TZL5.6

Query Match	6.0%;	Score 169.5;	DB 2;	Length 190;
Best Local Similarity	27.8%;	Pred. No. 2.5e-05;		
Matches	54;	Conservative	34;	Mismatches 57.

QY

382	RQVFAGAGNHLVD-ENFDELDYWTSLLEPKLVGTIVLMASVQSKRKRLRVYLHCTNT	440
12	ROSLIG-GNYELINTNETNPDPYSALITWPIIMCGRDILFMETTCCTT	

QY
441 DNRKYKEGDLTYAINLHNVT-----TKYLRLPYRPFNKQVDKYLRLPL 483

Dbb
67 ---RSQSG--ITVLLMNTLDNPPPTVVAVLKVETANSDEGRDHTTIVTTT-----|

484 GPHGLL-----SKSYVNLGLTLTKMVDQDTLPLEMEKPLRPSSSLGPAFS 528
||::| | | | | | | | : : :
116 GPNGVIOREERYH.TAKDGNTHSCMMITLVNQAICNVGGC-----: : :
Db

529 YSFFVIRNAKVAAC 542

176 IYFVHMRIIVYDAG 199

RESULT 4

Hypothetical protein MJ0670 - Methanococcus jannaschii
;Species: Methanococcus jannaschii
Date: 13-Sep-1996 #genome: mjan11

Accession: F04383
Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; G.
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; G.

Authors: Kaine, B. P.; Borodovsky, M.; Klenk, H. P.; Frazer, C. M.; Smith, H. O.; Borodovsky, M. A.

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;Accession: F64383
;Status: preliminary; nucleic acid sequence not shown; translation not shown
;Molecule type: DNA

```

Map position: REV596956-595886
Genetics: UNIPROT:Q58084; GB:U67514; NID:G2826304; PIDN:AAE
Cross-references: UNIPROT:Q58084; GB:U67514; NID:G2826304; PIDN:AAE

Query Match	4.0%	Score	112.5;	DB 2;	Length	356;
Best Local Similarity	21.2%	Pred	No	1.1		

126 ICKY-----GSPDVEEKLRLFWYQEQILLREHYQKKFNSTYRSSVD-----171

Db 14 IRKMYKINGKNEKDIKERLIKE-----LKEHVLEVTEBDGYTLTKAEDEEMMSKV 66
QY 172 -----VLTPFANGSGDLIFGLNALLRTADLQWSSNAQLLDYSSKGYNISWEIGNEP 226
Db 67 GALKKATYKFAKPS-----KITDL-----SNPK-VIDLCSGKGYNAIALHYNK 109
QY 227 NS-----FL-----KKADIFINGSQLEDYIQLHKLKSTF 258
Db 110 NAEIMWEICEBEVLFLTLFLDIPYKHEHIIKQKVEFYFN-KIGREY-----KSDY 159
QY 259 KNAKLYGPDVGQPRKRTAKMLKSFKAGGEVIDSVTHHHYINGRTAT--REDFINPDVL 316
Db 160 DNINLY---VGDARFIIKSDKKY-----NVFHDSPKPKDPTLYTYDFL----- 202
QY 317 DIFISVQKPVQVSTPRGKVMGETSSAYGAGAPLISDFPAGFMMLDLGLSARWG 376
Db 203 -----KEIYKQMEDN--GVLI-----SYSSAIPFSAALVDCGFVSESESVGRKKG 246
QY 377 IEVNRQVFFGAGNHLVDENFD-----PLPDYWLSLIFPKKLVGTQKVLMAVQGSXKR 429
Db 247 ITLAKNPKPKNRINENDEVERIALSVIALPYRDELISITKDKIIEDRERREKLEKLI 306
QY 430 KLRVYLHCTNTDNPYKESGDLTLVA--INLHNVTKYLRIPY 468
Db 307 KIGKYLSTQIKKGNIPBEILKIOKEDLNSSEIIKKMRLEKF 347

RESULT 5

T12094
beta-fructofuranosidase (EC 3.2.1.26) - fava bean
C1Species: Vicia faba (fava bean)
C1Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C1Accession: T12094
R1Weber, H.; Botisjuk, L.; Helm, U.; Buchner, P.; Mobus, U.
Plant Cell 7, 1835-1846, 1995
A1Title: Seed coat-associated invertases of Fava bean control both unloading and storage
A1Reference number: Z17416; MUID:96093423; PMID:8535137
A1Accession: T12094
A1Status: preliminary; translated from GB/EMBL/DBJ
A1Molecule type: mRNA
A1Residues: 1-575 <WEB>
A1Cross-References: UNIPROT:Q43855; EMBL:Z35162; NID:9861154; PIDN:CAA84526.1; PID:98611
A1Experimental source: cv. Fr1bo, seed coat
C1Genetics:
A1Gene: CMINV1
C1Superfamily: beta-fructofuranosidase
C1Keywords: cell wall; glycoprotein; glycosidase; hydrolase

Query Match 3.9%; Score 11.5; DB 2; Length 575;
Best Local Similarity 21.4%; Pred. No. 2.7; Indels 109; Gaps 19;
Matches 72; Conservative 48; Mismatches 107; Indels 109; Gaps 19;
QY 46 QEPHLVLS-----PSFLSVTIDANLATDPRFLILGSPKRLTLARGLS-----P 89
Db 228 KPIHISAKRTGMECEPDFYPSVLEGKNGLD--LSMMGNNVGHVKNLSIDITREYETIG 285
QY 90 AYLR-----FGTKTDF-----LIFDPKESTFEERSTW---OSQVNG 124
Db 286 TYLQNDQKXIPDKTSEDDGGLRVDYGNFYAKSPFDDPK---NRIITWGNANSDTYE 341
QY 125 DICKG---SIPPDV-----EKKRLLEWPYOEQLLR-----EHYOKFKNSTYSRSRV 170
Db 342 DDVKGMAGIOAIPTFTWLDSSRRQR--QMPVEELNRLRGQVEMKRLKKGKY---L 396
QY 171 DVLVTFPANGSGDLIFGLNALLRTADLQWSSNAQLLDYSSKGYNISWEIGNEPNSFL 230
Db 397 EYKGITASQADVEVTFSSFLDKAEAFDPMENAE---DLCAQKSGKVGAGV--PFGIL 451
QY 231 KKADIFINGSQLEDYIQL-----HKL-----RSTPKNAKLYGP-----DV 268
Db 452 TLA-----SKLDEETYSVFFRVFKANKGKILMKSDAASSLNLRELKPSFAGFVNDL 505
QY 269 GQPRRTAKMLKSFKAGGEVIDSVTHHHYINGRT 304

Db 506 GNNKKLSIRSL-----IDHSVSESFVGVGRT 531

RESULT 6

T10666
hypothetical protein F6E21.40 - Arabidopsis thaliana
C1Species: Arabidopsis thaliana (mouse-ear cress)
C1Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C1Accession: T10666
R1Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro
submitted to the Protein Sequence Database, June 1999
A1Reference number: Z16533
A1Accession: T10666
A1Molecule type: DNA
A1Residues: 1-670 <BY>
A1Cross-References: UNIPROT:Q9M090; EMBL:AL049914; GSPDB:GM000062; ATSP:F6E21.40
A1Experimental source: cultivar Columbia; BAC clone F6E21
C1Genetics:
A1Map position: 4
A1Intons: 47/3; 87/1; 123/3; 203/3; 230/2; 255/3; 284/3; 305/1; 335/3; 347/3; 370/3; 39
C1Superfamily: Schizosaccharomyces pombe negative regulator of mitosis bkl1

Query Match 3.9%; Score 11; DB 2; Length 670;
Best Local Similarity 22.4%; Pred. No. 3.7; Indels 156; Gaps 33;
Matches 123; Conservative 77; Mismatches 194; Indels 156; Gaps 33;

QY 51 LVSPSFLSVTIDANLATDPRFLILGSPKRLTLARGLSPAY--LRFGKTDFLIIPDK- 107
Db 47 LVDPSPRSLVEGN-GVDTQVLPVCGSDLV-----LSPSQWSSHVVGKISSWIDLSD 99
QY 108 -----KESTFEERWYQSONNODICKXGSIIPDVEKRLRWEPYQEQLLREHYQKKFK 161
Db 100 EYLRMDSTTLKQETAMATHLSLQMCB-----PD-----LTPHLAGL 139
QY 162 NSTYSSRSV---DVLX-----TFANCS--GLDLIFGLNALLRTADLQWSSNAQL 207
Db 140 RVSCCRSSFIDETFLYITFNQALTFCGSSILFCLNVISALKMLRWPLVK---SEGDSM 196
QY 208 LDYSSKGYNISWEIGN-----EPNSFLKKA-DIFIN-----GSQLEDYIQLHKL 253
Db 197 DD--TSEGLNDSWEIEMNSFRLLCEHDSKLSVALDVLSTLPSETSLGRWVGES--VPAALIS 253
QY 254 RSTFKNAKLYGPDVGP--RRKTAKMLKSPF--KAGGEVIDSVTHHHYINGRTATREDF 310
Db 254 TDAFLTNAR-----GYFCLSRHQKLIAGFPDHAQVVICGKPVHNLQKPLDSSSGTE 307
QY 311 INPDVLDFISSVQKPVQVSTPRGKVMGETSSAYGAGAPLISDFPAGFMMLDKLG 370
Db 308 KNP--LRIVLYDVVALFQKMSLSQERIEIGYRFLQAPLMDNLEAQYETFE--- 362
QY 371 LSARNGIEVNRQVFFGAGNHLVDENFDPLPDYWLSLIFKKLVGTXYLM----- 420
Db 363 ---RDSVXIQYQ---RAVERKALVDR---VPDEKASEL-----TVLMMVVGAGRGPLY 406
QY 421 -ASVQSGSR--RKLRVYLHCTNTDNPYKESGDLTLVAIINLHNVTK-----YLRLPY 468
Db 407 RASLOAAEETDRKLVY--AVEKNPN-----AVTLHNLVMEGMEDEVYTIISCDM 455
QY 469 PFSN--KQVDKYLRLPLPGHLSKSVOLNGLTLTMVDDQTLPLPM---EKPLRPGSSIG 523
Db 466 RFWNPRPQADILVSLSSFG-----DNEISPECLDGAQRRLK--DGIS 498
QY 524 LPAFSFFV 533
Db 499 IPS-SYTSFI 507

RESULT 7

S32961
hypothetical protein YBR259w - yeast (Saccharomyces cerevisiae)
N1Alternate names: hypothetical protein YBR127

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Qy      78 PKLRTIARGLSPA-----YLRFGGTYKTDLIFDPKKKESTEEKSYSOMOSV-NODIC 127
Db      1447 PRVDLIERLTITSENAHKAECCLINIRAMNOIARLVNMSGESASAPRPTITWNNNFNOJILD 1506
Qy      128 KQGSIPDPVEEKLK-----LEMPYOQLLREHYQCKFKNSTYRSRSEVDULYTFAN 178
Db      1507 QYMSASDIEQOFALSAENMRSIDAMRRELITKN-----KATMDILHTSAR 1555
Qy      179 CGGLIIFGLNL-----LRTADLQ-----WNSNAQLLDYCSKGNI 218
Db      1556 AS-LDVLKQAKTLEAAYTLNTVQLQIMCTTLHPGSEFGPMGLINVL-----DTHAFPL 1609
Qy      219 SW-ELGNEENSLFKKADIFINGSQIGEDYIQLHKLKSTFKNAKLGPDPGQPRKRTAK 277
Db      1610 GWIETSEEQYSSNESSEADIDPRQLEDAIILLQELKTEFFWMA-----RELLAL 1659
Qy      278 MKSLFKAGGEYID-SVTMHHYILNGRTAREDFLMPDVLDFISSVOKVQVVESTRPG 336
Db      1660 FLKAITTFEQIYQVACTEKTIVTLANKLAKR-----PLQ-ERYIQLVLPYRPG 1706
Qy      337 K-----KWLGETSAYGGGAPILLSDTFAAG-----FMWLDK 368
Db      1707 KYGLEPDMKNNSGPERRWL-----PLFIATLVKQNVDFDIETNLSLWQS 1755

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QY      369  LLSLSAR-WGIEVVMQVFFGAGNYHL--VDENDDLPDYLSL-LFCKLYG--TKVL--- 419
Db      1756  IIKPMRFGLGYETVYLAELVLOQRGLPLPLAADVSAKGMTPDYNIHLDFSRALHYMKRLRG 1815
QY      420  -----MASVQSK-----RRKLRYVLIHCTNTNDNPRYKEGDDLTVYAINLHNATKYL 464
Db      1816  ATPPAGVTSASASTGSSSAQSIIRQRPEPSH----- 1847
QY      465  RLPPFPSSKQVDRKYLRLPG-----PGLLSKSYQLNGLTIKMD-- 504
Db      1848  TLQLAMTINIKQLFLRLSLADPTASSTEEHRYMAFTGGLLS-LIKSGVGIVVDSF 1906
QY      505  -----DQTLPPIMEKRLRPG-----SSLGLPAPSYSF-FVIRNAKYA 540
Db      1907  FLTPSDVSYPFLQDPQLHTAGIMAYGVRLSEKQVPAASGLFWLFFNNFKYA 1957

RESULT 9
E91031
probable outer membrane protein EC83221 [imported] - Escherichia coli (strain O157:H7, su
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: E91031
R:Hayashi, T.; Makino, K.; Omishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Ganawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genor
A:Reference number: A59629; MUID:21156231; PMID:11258796
A:Accession: E91031
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-879 <HAY>
A:Cross-references: UNIPROT:G8XCP4, GB:BA000007, PIDs:BA536644.1; PID:913362691; GSPDB:GI
C:Geneticals:
C:Experimental source: strain O157:H7, substrain RIMD 0509952
A:Gene: EC83221

Query Match      3.9%; Score 109.5; DB 2; Length 879;
Best Local Similarity 20.1%; Pred. No. 7.3; 208; Indels 241; Gaps 33;
Match 130; Conservative 68; Mismatches 241; Gaps 33;

QY      52  VSPFLSTVIDANLTDPREFILILGSPKRLTLARGLSPAYLRGGRYTDPLIDPKKEST 111
Db      20  MSGSYVNAEMIEIOFDSRFLETKGPTKI-DLKRFSSQGVBERG--KYNLOVONKROPLT 76

```

0y	112	FEERSYQWQVNO	DICTGSI	PPDVEBKL	-----	RLBMPYQ	OBQLL	REHYQ	KERN	163
0b	77	BEYDIYVASE	NDSTYAC	LPELVA	OFLKED	VAKNI	OWIH	DGCL	KRGQLE	130

A:Gene: ADE1; SPDB:SPBC405.01

A:Map position: 2

C:Superfamily: Saccharomyces cerevisiae ADE5 multifunctional protein; phosphoribosylamin

C:Keywords: cyclo-ligase; purine nucleotide biosynthesis

F/5-425/Domain: phosphoribosylamine-glycine ligase homology <PGL>

F/439-767/Domain: phosphoribosylformylglycinamide cyclo-ligase homology <PFCU>

Query Match 3.7% Score 104.5; DB 1; Length 788;

Best Local Similarity 27.7%; Pred. No. 15; Mismatches 114; Indels 33; Gaps 11;

Matches 70; Conservative 36; Mismatches 114; Indels 33; Gaps 11;

QY 237 HYLNGRTATRE--DFLNPDV-LDIFISSVQKVFQVEST--RPGKRWLGERTSAY---- 348

DB 424 HVALNPKKTRILLYENSGVSDNGNEFQRIKOLVSTRPADADIGCGIFDLKQ 483

QY 349 -GGAPLL-SDTFANGFMWLDKLGSLAR--NGEIVNRQVFFGAGNYHLVDENPDL--P 402

DB 484 AGMNDPLVSATDVGSKLLIALSLNKHDTVGIDLVAMNV-----NDLVVQGAEPILFL 537

QY 403 DYWLSLFRKLVGTGKVLMAVSGSKRRKLRVYLHCTNTDNPRYKEGDLTLVAINLHNTX 462

DB 538 DVFATGSLDKVTSFVGVGKCKQAGCALVGSETSEMPGLYHDGHYDANGTSVGAISR 597

QY 463 YLRLEPFSNKQVDKYLRLRPLGPHGLSKSVQNLGLTL--KMVD----DQTLPLMERPL 516

DB 598 DDILPKPESFSGDILL-----GLASDGVHNSNGSLVRKIVEYSDLEYTSVCPMDKNV 650

QY 517 RFGSSLGLPAPSY 529

DB 651 RLGDSLILPTRY 663

RESULT 15

F70411 adenylosuccinate synthetase - Aquifex aeolicus

C:Species: Aquifex aeolicus

C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C:Accession: F70411

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O

V. Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: F70411

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-432 <AQP>

A:Cross-references: UNIPROT:O67321; GB:AE000733; NID:g2983720; PIDN:AAC07286.1; PID:g298

A:Experimental source: strain VPS

C:Genetics:

A:Gene: pura

C:Superfamily: adenylosuccinate synthase

Query Match 3.7% Score 104; DB 2; Length 432;

Best Local Similarity 23.9%; Pred. No. 6.4; Mismatches 128; Indels 138; Gaps 22;

Matches 96; Conservative 39; Mismatches 128; Indels 138; Gaps 22;

QY 15 LLLGLPLGLSPGALPRPAQADVVDL-----FFTQEPHLVSPS 55

DB 51 ILHLPTGILHBAHVAGVIAQGM-VVDLEVLHKEVKNLBEKGIYKERLFISDRAHLVMPY 109

QY 56 FLSTVITDNLATDPRFLILGSPK--LRTLAGLSPAYL-RFGCTKTDPLIFDPKKESTF 112

DB 110 H-----KLDSLFKKKGIGITLRLGIGAPAYFKYG--RKGIRISDLKDEKRF 154

QY 113 EERSYQSQVNODICKYGSIPDVEEK-----RLTEWPYOEQLLRHYQKFKNSTY 165

DB 155 -----YTLLEDNDLPK-----NICEKVCCEKFDLDINOIYEQI-----RYFEFEKENV- 199

QY 166 SRSSVDVLYTFANCSGLDILFGLNALRTADL-----QNNSSNAQLLDYCSSKGYNISWE 221

DB 200 ---VDLLRFNTQKGSVLFEGAGQGTILDVDWGTVPYVYSSNASAL-----GLSNG 246

QY 222 LGNEPNSFLKKADIFING-----SQL-GE DYIOLHKLRLKSTFNKAKLYG 265

DB 247 TGMPPKYF---SDAFILGVAKAYTTRVGEFPFTELKGESEKRLREL-----GGEYG 295

QY 266 PDVGQPRR---KTAKMLKSLKAGGEVIDSVTHHYLYNGRTATREDPLN----- 313

DB 296 STTGRPRRCGWLIDVALKXAVQVNG-----LDGFVITGLDVLDTFDEVKCVVA 343

QY 314 -----DVIDFISSVQKVFQY--VSTRPGKKWLGERTSA 347

DB 344 YELDGEVIDYFPASYSBLIRKVPYKTLKG--WKGSTKGA 381

Search completed: February 28, 2005, 05:53:41

Job time : 48 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2005, 05:52:46 ; Search time 180 Seconds
(without alignments)
1544.772 Million cell updates/sec

Title: US-10-786-149-2

Perfect score: 2842

Sequence: 1 MLRSKAPLPPLMLLLGP.....LPAPSPFVIRNAKVAACI 543

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2838	99.9	543	2	Q9Y251
2	2817	99.1	545	2	Q9UL39
3	2282	80.3	545	2	Q9MYT0
4	2150	75.3	535	2	Q8K3K3
5	2140	75.3	535	2	Q6Y9Z1
6	2135	75.1	536	2	Q71RP1
7	2123	74.7	536	2	Q9QZP8
8	1645.5	57.9	523	2	Q9QYK5
9	1154.5	40.6	592	2	Q9HB37
10	1146.5	40.3	592	2	Q8WQ2
11	1015.5	35.7	548	2	Q8WQ1
12	936.5	33.0	534	2	Q9HB38
13	897.5	31.6	480	2	Q9HB39
14	696	24.5	515	2	Q8T108
15	416	14.6	521	2	Q8SDA1
16	416	14.6	543	2	Q9FF10
17	404	14.2	559	2	Q89F99
18	392.5	13.8	544	2	Q8H615
19	381	13.4	527	2	Q9LRC8
20	379	13.3	541	2	Q691T5
21	364	12.8	537	2	Q70YJ3
22	363	12.8	536	2	Q9FZP1
23	352.5	12.4	516	2	Q9FLK8
24	352.5	12.4	539	2	Q8L608
25	350.5	12.3	529	2	Q6ZJ62
26	169.5	6.0	190	2	Q8Z604
27	160	5.6	935	2	Q9YE79
28	141	5.0	559	2	Q7SF80
29	136.5	4.8	463	2	Q63T97
30	130.5	4.6	493	2	Q9HK01
31	122.5	4.3	408	2	Q9HE21

32	122.5	4.3	408	2	Q9HE22	Q9he22 phanerochae
33	116.5	4.1	619	2	Q40966	Q40966 measles vir
34	114.5	4.0	1167	2	Q869K5	Q869K5 dictyosteli
35	114	4.0	398	2	Q72RP7	Q72rp7 leptospira
36	114	4.0	398	2	Q8F410	Q8f410 leptospira
37	113.5	4.0	617	2	Q83295	Q83295 measles vir
38	113.5	4.0	1829	2	Q9KH44	Q9kh44 pantoea agg
39	113	4.0	390	2	Q8TPH7	Q8tph7 methanosarc
40	112.5	4.0	356	1	Y670.METUA	Y670.METUA
41	112.5	4.0	617	2	Q83647	Q83647 measles vir
42	112	3.9	732	2	Q7MSD4	Q7msd4 wolinnella b
43	111.5	3.9	493	2	Q979W0	Q979w0 thermoplasm
44	111.5	3.9	575	2	Q43855	Q43855 victa faba
45	111.5	3.9	617	2	Q40991	Q40991 measles vir

ALIGNMENTS

RESULT 1

ID	Q9Y251	PRELIMINARY	PRT	543 AA.
AC	Q9Y251			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DT	25-OCT-2004	(TREMBLrel. 28, Last annotation update)		
DE	Heparanase.			
GN	Name=HPA; Synonyms=HPSE;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=99332149; PubMed=10395326;			
RA	Hulett M.D., Freeman C., Hamdorf B.J., Baker R.T., Harris M.J.,			
RA	Parish C.R.;			
RT	"Cloning of mammalian heparanase, an important enzyme in tumor			
RT	invasion and metastasis."			
RT	Nat. Med. 5:803-809(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=99335379; PubMed=10405343; DOI=10.1006/bbrc.1999.0962;			
RA	Kusie P.H., Holmes J.D., Ludwig D.L., Patel S., Navarro E.C.,			
RA	Seddon A.P., Giorgio N.A., Bohlen P.;			
RT	"Cloning and functional expression of a human heparanase gene."			
RT	Biochem. Biophys. Res. Commun. 261:183-187(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99377052; PubMed=10446189; DOI=10.1074/jbc.274.34.24153;			
RA	Toyoshima M., Nakajima M.;			
RT	"Human heparanase. Purification, characterization, cloning, and			
RT	expression."			
RT	J. Biol. Chem. 274:24153-24160(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Pancereas;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strasberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner T., Shermen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh P.,			
RA	Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carinci P., Prange C.,			
RA	Baba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Boesk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywiński M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RT Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."/
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.,
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Vlodavsky I., Friedman Y., Bikin M., Aingorn H., Arzmon R.,
RA Ishaï-Michaeli R., Bitan M., Pappo O., Peretz T., Michael I.,
RA Spector L., Becker I.,
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165154; AAD45379.1; -
DR EMBL; AF152376; AAD45669.1; -
DR EMBL; AF155510; AAD54941.1; -
DR EMBL; BC051321; AAH51321.1; -
DR EMBL; AF144325; AAD41342.1; -
DR GO; GO:0004566; F-beta-glucuronidase activity; TAS.
DR GO; GO:0006029; P-proteoglycan metabolism; TAS.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
DR CHAIN 158 543 heparanase.
SQ SEQUENCE 543 AA; 61176 MW; AD262EC267334AB2 CRC64;

Query Match 99.9%; Score 2838; DB 2; Length 543;
Best Local Similarity 99.8%; Pred. No. 1.9e-204;
Matches 542; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVDLDFTQEPRLHLVSPSFLSVT 60
Db 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVDLDFTQEPRLHLVSPSFLSVT 60
QY 61 IDANLATDPRFLILGSPKRLTLARGLSPAYLRFGGTDTFLIPDKKESTFEERSYWS 120
Db 61 IDANLATDPRFLILGSPKRLTLARGLSPAYLRFGGTDTFLIPDKKESTFEERSYWS 120
QY 121 QVNODICKYGSIPDVEEKLRLMPYQEQLLREHYQKKFNKSTYSRSVDVLYTFANCS 180
Db 121 QVNODICKYGSIPDVEEKLRLMPYQEQLLREHYQKKFNKSTYSRSVDVLYTFANCS 180
QY 181 GIDLIFGLNALIRTAQLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINCS 240
Db 181 GIDLIFGLNALIRTAQLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINCS 240
QY 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTMHHY 300
Db 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTMHHY 300
QY 301 NGRTATREDPLNDVDLIFISSYQKVPQVESSTRPKKWLGETSSAYGGAPLLSDTFA 360
Db 301 NGRTATREDPLNDVDLIFISSYQKVPQVESSTRPKKWLGETSSAYGGAPLLSDTFA 360
QY 361 AGFWMLDKLGLSARMGIEVVMROVFGAGNYHLVDENPDLDPYWLSTLFLKKLVGTVKM 420
Db 361 AGFWMLDKLGLSARMGIEVVMROVFGAGNYHLVDENPDLDPYWLSTLFLKKLVGTVKM 420
QY 421 ASVQSGRRKRLRYVLIHCTNDNPRYKSGDLTLVAINAHVTYKRLPYPSNQVDKYLL 480
Db 421 ASVQSGRRKRLRYVLIHCTNDNPRYKSGDLTLVAINAHVTYKRLPYPSNQVDKYLL 480
QY 481 RPLGPHGLSKSVQNLGLTLKMWDDQTLPLMEKPLRPSSGLPAFSYFFVIRNAKYA 540
Db 481 RPLGPHGLSKSVQNLGLTLKMWDDQTLPLMEKPLRPSSGLPAFSYFFVIRNAKYA 540
QY 541 ACI 543
Db 541 ACI 543

RESULT 2
Q9ULJ39
ID Q9ULJ39 PRELIMINARY; PRT; 545 AA.
AC Q9ULJ39;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Heparanase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20229546; PubMed=10764835; DOI=10.1093/glycob/10.5.467;
RA Dempsey L.A., Plummer T.B., Coombes S.L., Platt J.L.,
RT "Heparanase expression in invasive trophoblasts and acute vascular
RT damage."/
RL Glycobiology 10:467-475 (2000).
DR EMBL; AF084467; AAD54516.1; -
DR Genew; HGNC:5164; HPSE.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
DR CHAIN 158 543 heparanase.
SQ SEQUENCE 545 AA; 61417 MW; 67B80ACD73C5A9A1 CRC64;

Query Match 99.1%; Score 2817; DB 2; Length 545;
Best Local Similarity 99.4%; Pred. No. 7.1e-203;
Matches 542; Conservative 1; Mismatches 0; Indels 2; Gaps 2;

QY 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVDLDFTQEPRLHLVSPSFLSVT 58
Db 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVDLDFTQEPRLHLVSPSFLSVT 58
QY 59 VTIDANLATDPRFLILGSPKRLTLARGLSPAYLRFGGTDTFLIPDKKESTFEERSYWS 118
Db 61 VTIDANLATDPRFLILGSPKRLTLARGLSPAYLRFGGTDTFLIPDKKESTFEERSYWS 120
QY 119 QSVNODICKYGSIPDVEEKLRLMPYQEQLLREHYQKKFNKSTYSRSVDVLYTFAN 178
Db 121 QSVNODICKYGSIPDVEEKLRLMPYQEQLLREHYQKKFNKSTYSRSVDVLYTFAN 180
QY 179 CSGLDIFGLNALIRTAQLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFIN 238
Db 181 CSGLDIFGLNALIRTAQLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFIN 240
QY 239 GSQLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTMHHY 298
Db 241 GSQLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSLFKAGGEVIDSVTMHHY 300
QY 299 YINGRTATREDPLNDVDLIFISSYQKVPQVESSTRPKKWLGETSSAYGGAPLLSDT 358
Db 301 YINGRTATREDPLNDVDLIFISSYQKVPQVESSTRPKKWLGETSSAYGGAPLLSDT 360
QY 359 FAAGFWMLDKLGLSARMGIEVVMROVFGAGNYHLVDENPDLDPYWLSTLFLKKLVGTVKM 418
Db 361 FAAGFWMLDKLGLSARMGIEVVMROVFGAGNYHLVDENPDLDPYWLSTLFLKKLVGTVKM 420
QY 419 LMAVSQSGRRKRLRYVLIHCTNDNPRYKSGDLTLVAINAHVTYKRLPYPSNQVDKY 478
Db 421 LMAVSQSGRRKRLRYVLIHCTNDNPRYKSGDLTLVAINAHVTYKRLPYPSNQVDKY 480
QY 479 LRLPLGPHGLSKSVQNLGLTLKMWDDQTLPLMEKPLRPSSGLPAFSYFFVIRNAKYA 538
Db 481 LRLPLGPHGLSKSVQNLGLTLKMWDDQTLPLMEKPLRPSSGLPAFSYFFVIRNAKYA 540
QY 539 VAACT 543
Db 541 VAACT 543

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RESULT 3
Q9MYX0 PRELIMINARY; PRT; 545 AA.
ID Q9MYX0
AC Q9MYX0
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Heparanase.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=21176669; PubMed=11277877;
RA Kizaki K., Nakano H., Nakano H., Takahashi T., Imai K., Hashizume K.;
RT "Expression of heparanase mRNA in bovine placenta during gestation.";
RL Reproduction 121:573-580(2001).
DR EMBL; AF281160; AAF87301.2; -;
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; I.
SQ SEQUENCE 545 AA; 61076 MW; FAF4BDFD855B933 CRC64;

Query Match 80.3%; Score 2282; DB 2; Length 545;
Best local similarity 79.8%; Pred. No. 1,1e-162;
Matches 435; Conservative 35; Mismatches 73; Indels 2; Gaps 1;

QY 1 MLRSKPALPPPLML--LGLPLGLSPGALPRPAQADVLDLPTQEPRLHLVSPFLS 58
DB 1 MLACRKPELRPPLLLPLGLPLGLGCSGPTAAAAFADDALEPFTERRPLHLVSPFLS 60
QY 59 VTIDANLATDRPRLILLGSPKLTARGLSPAYLRFGSTKTDLFIDPKKSTPEREY 118
DB 61 FTIDANLATDRPRLFFFLGSSSKLTARGLAPAYLRFGNKDFLIDPKKPAPEERSY 120
QY 119 QSOVNODCKYGSIPDVVEEKLRLMPYOEOLREHYOKKSTYRSYSDVLYTPAN 178
DB 121 LSGNSODCKSGSLPSDVEEKLRLMPYOEOLREHYOKKSTYRSYSDVLYTPAN 180
QY 179 CSGDLIFGLNALRTADLQWNSNAQLLDYCSSSKYNIEMELGNEPSEFLKADIPIN 238
DB 181 CSGDLIFGLNALRTADLQWNSNAQLLDYCSSSKYNIEMELGNEPSEFLKADIPIN 240
QY 239 GSQGEDYIQHLKLRKSTFKNAKLYGPDVQPRPKTKMLKSPFKAGGEYIDSTWYHY 298
DB 241 GROLGEDIFFRKLLGSAFKNAKLYGPDIGQPRNTYKMLKSPFKAGGEYIDSTWYHY 300
QY 299 YLNRTRAREDFLNPDDVDFIFSSVQKYFOVESRPRGKYWLGFTSAGGGAFLISDT 358
DB 301 YVNGRIATKEDPLNDDLDFTLSSVQKTRIVKTRPKRWLGFTSAGGGAFLISNT 360
QY 359 FAAGFMWLDKLGSARMGIEVVMROVFTGAGNYHLVDENPDLDPYWLSLFLPKLVGTV 418
DB 361 FAAGFMWLDKLGSARMGIEVVMROVFTGAGNYHLVDENPDLDPYWLSLFLPKLVGTV 420
QY 419 LMASVQSKRRRLRYLHCTNTDNPRYKGGDTLYAIVLHANTYKRLPYPPSKQVDY 478
DB 421 LMASVQSKRRKFRYLYHCTNTKPRYKGGDTLYAIVLHANTYKRLPYPPSKQVDY 480
QY 479 LLRLPGHGLSKSVQNLGLTLKMWDDOTLPRLMKEKRLPPSSGLPAPSYSPFIRNAK 538
DB 481 LKPSGTGGLSKSVQNLGLTLKMWDDOTLPRLMKEKRLPPSSGLPAPSYSPFIRNAK 540
QY 539 VAACI 543
DB 541 VAACI 545

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Q8K3K3;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Heparanase (Mus musculus 0 day neonate thymus cDNA, RIKEN full-length
DE enriched library, clone:A430101M04 product:heparanase, full insert
DE sequence).
CN Name=Hpsa; Synonyms=Hpa, Hspe;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB;
RA Miao H.-Q., Navarro E., Patel S., Sargent D., Koo H., Wan H.,
RA Plata A., Zhou Q., Ludwig D., Bohlen P., Kissele P.;
RT "Cloning, expression, and purification of mouse heparanase.";
RL Protein Expr. Purif. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto K., Matsuno H., Sakaguchi S., Ikegami T., Kaishogi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed capillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akiyama T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Koda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

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RA Nishi K., Nomura K., Numazaki R., Ohno M., Ono S., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai C., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takeku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RU Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=STJ/J; TISSUE=Spleen;
 RA Hallet M.D., Wang J., Hornby J.R., Freeman C., Pagler E., McHenry J.,
 RA Parish C.R.,
 RU Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY077467; AAL76083.1; -
 DR EMBL: AK040471; BAC30600.1; -
 DR EMBL: AF359507; AA015188.1; -
 DR MGD: MGI:1343124; Hpaee.
 DR GO: GO:0005788; C.electracellular matrix (sensu Metazoa); TAS.
 DR InterPro: IPR005199; Glyco_hydro_79N.
 DR Pfam: PF03662; Glyco_hydro_79N.
 DR SEQUENCE 535 AA; 60065 MW; 6E73A8302FB8A0DF CRC64;

Query Match 75.7%; Score 2150; DB 2; Length 535;
 Best local Similarity 76.6%; Pred. No. 8.9e-153;
 Matches 407; Conservative 51; Mismatches 73; Indels 0; Gaps 0;

QY 13 LMLLLGPIGLPSGALPRPAQADVDVDFFTQEPHLIVSPSPFLSVTTIDANLATDPRFL 72
 DB 5 LILMLMGPPLGALAGAPAGTAPTDVDFEFTYKRPURSVSPFLSTITDASLATDPRFL 64
 QY 73 ILGSPKRLTARGLSPAYIRFGGKTDFLIPDKKESTFEERSYVQSQVNDICKYGS1 132
 DB 65 TFLGSPRLALARGSPAYIRFGGKTDFLIPDKKESTFEERSYVQSQVNDICKRSEPV 124
 QY 133 PPVBEKRLRLEWYQEOULLREHYOKFKFNSTYSSRSVDVLYTFANCSGLDIFGINALL 192
 DB 125 SAALVRLQVEMPFQELLLRQYQKEFNSTYSSRSVDVLYTFANCSGLDIFGINALL 184
 QY 193 RTADLQNNSSNAQLLDYCSSKGNISWELGNEPNSFLKKAIDIFINGSLQGEDYIOLHKL 252
 DB 185 RTPDLRNNSSNAQLLDYCSSKGNISWELGNEPNSFWKKAHLLIDGLQGEDYFVLAHKL 244
 QY 253 LRKSTPKNAKLYGPDVGGPRKRTAKMLKSPFKAGGEVIDSVTHHHYINGRTATREDFLN 312
 DB 245 LQRSAPQNAKLYGPDVGGPRKRTAKMLKSPFKAGGEVIDSVTHHHYINGRTATREDFLN 304
 QY 313 PDVIDFISSVQKVFQVVESTRPGKRWLGETSSAYGGAPLSDTPAAGFMWLDKLGIS 372
 DB 305 SDVLDFTILSYQKILKVTKEITPGKKWLGETSSAYGGAPLSDTPAAGFMWLDKLGIS 364
 QY 373 ARMGIEVVMRQVFPAGNYHLVDENFDPLPDYWSLFPKLVGTGKVLMAVQSGSKRRKLR 432
 DB 365 AQMGIEVVMRQVFPAGNYHLVDENFDPLPDYWSLFPKLVGTGKVLMAVQSGSKRRKLR 424
 QY 433 VYLHCTNDNPRYKSGDLTLVAIINLHNTKYRLPYFPNSNKQVQKYLRLPGPHGLSKS 492
 DB 425 VYLHCTNVYHPRYQSGDLTLVAIINLHNTKYRLPYFPNSNKQVQKYLRLPGPHGLSKS 484
 QY 493 VOLNGILTKMVDQTLPLMEKPLRPGSSSLGAPASYSFFVIRNAKVACI 543
 DB 485 VOLNGILTKMVDQTLPLMEKPLRPGSSSLGAPASYSFFVIRNAKVACI 535

RESULT 5
 O6YGZ1 PRELIMINARY; PRT; 535 AA.
 AC O6YGZ1;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hepatranase.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22841152; PubMed=12837765; DOI=10.1074/jbc.M00925200;
 RA Gong F., Jench P., Galvis M.L.E., Vlodevsky I., Horner A., Lindahl U.,
 RA Li J.P.,
 RT "Processing of macromolecular heparin by heparanase."
 RU J. Biol. Chem. 278:35152-35158 (2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Li J.-P., Gong F., Lindahl U.;
 RU Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY151051; AAN41636.1; -
 DR GO: GO:0005578; C.electracellular matrix (sensu Metazoa); TAS.
 DR InterPro: IPR005199; Glyco_hydro_79N.
 DR Pfam: PF03662; Glyco_hydro_79N.
 DR SEQUENCE 535 AA; 59992 MW; 3748AB3795C718A CRC64;

Query Match 75.3%; Score 2140; DB 2; Length 535;
 Best local Similarity 76.6%; Pred. No. 5e-152;
 Matches 407; Conservative 50; Mismatches 74; Indels 0; Gaps 0;

QY 13 LMLLLGPIGLPSGALPRPAQADVDVDFFTQEPHLIVSPSPFLSVTTIDANLATDPRFL 72
 DB 5 LILMLMGPPLGALAGAPAGTAPTDVDFEFTYKRPURSVSPFLSTITDASLATDPRFL 64
 QY 73 ILGSPKRLTARGLSPAYIRFGGKTDFLIPDKKESTFEERSYVQSQVNDICKYGS1 132
 DB 65 TFLGSPRLALARGSPAYIRFGGKTDFLIPDKKESTFEERSYVQSQVNDICKRSEPV 124
 QY 133 PPVBEKRLRLEWYQEOULLREHYOKFKFNSTYSSRSVDVLYTFANCSGLDIFGINALL 192
 DB 125 SAALVRLQVEMPFQELLLRQYQKEFNSTYSSRSVDVLYTFANCSGLDIFGINALL 184
 QY 193 RTADLQNNSSNAQLLDYCSSKGNISWELGNEPNSFLKKAIDIFINGSLQGEDYIOLHKL 252
 DB 185 RTPDLRNNSSNAQLLDYCSSKGNISWELGNEPNSFWKKAHLLIDGLQGEDYFVLAHKL 244
 QY 253 LRKSTPKNAKLYGPDVGGPRKRTAKMLKSPFKAGGEVIDSVTHHHYINGRTATREDFLN 312
 DB 245 LQRSAPQNAKLYGPDVGGPRKRTAKMLKSPFKAGGEVIDSVTHHHYINGRTATREDFLN 304
 QY 313 PDVIDFISSVQKVFQVVESTRPGKRWLGETSSAYGGAPLSDTPAAGFMWLDKLGIS 372
 DB 305 SDVLDFTILSYQKILKVTKEITPGKKWLGETSSAYGGAPLSDTPAAGFMWLDKLGIS 364
 QY 373 ARMGIEVVMRQVFPAGNYHLVDENFDPLPDYWSLFPKLVGTGKVLMAVQSGSKRRKLR 432
 DB 365 AQMGIEVVMRQVFPAGNYHLVDENFDPLPDYWSLFPKLVGTGKVLMAVQSGSKRRKLR 424
 QY 433 VYLHCTNDNPRYKSGDLTLVAIINLHNTKYRLPYFPNSNKQVQKYLRLPGPHGLSKS 492
 DB 425 VYLHCTNVYHPRYQSGDLTLVAIINLHNTKYRLPYFPNSNKQVQKYLRLPGPHGLSKS 484
 QY 493 VOLNGILTKMVDQTLPLMEKPLRPGSSSLGAPASYSFFVIRNAKVACI 543
 DB 485 VOLNGILTKMVDQTLPLMEKPLRPGSSSLGAPASYSFFVIRNAKVACI 535

RESULT 6
 Q7IRP1 PRELIMINARY; PRT; 536 AA.
 AC Q7IRP1;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hepatranase.
 GN Name=Hape;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Hulett M.D., Wang J., Hornby J.R., Freeman C., Pagler E., McHenry J.,
 RA Parish C.R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF359508; AAQ15189.1; -
 DR InterPro; IPR005199; Glyco_hydro_79N.
 DR Pfam; PF03662; Glyco_hydro_79n; 1.

SO SEQUENCE 536 AA; 60479 MW; C434E04CF536EAD CRC64;

Query Match 75.1%; Score 2135; DB 2; Length 536;
 Best Local Similarity 76.1%; Pred. No. 1.2e-151;
 Matches 407; Conservative 50; Mismatches 78; Indels 0; Gaps 0;

QY 9 LPPRLMLLLGLPLGSPGALPRPAQADVDLDPFQGEPLHLVSPSLSTVIANLATD 68
 DB 2 LRPILLMLWGRGLALTGTPAGTAPTKOVVDLEFRTKLFQSVSPSLSTITIASLATD 61
 QY 69 PRFLILGSPRLRLTARGLSPAYLRFGGTKTDPLIFDPKKESTFEERSYWSQVNDICK 128
 DB 62 PRFLIFLGSPLRLALARGSPAYLRFGGTKTDPLIFDPKKESTFEERSYWSQVNDICK 121
 QY 129 YGSIIPDVEEKLRLMEPYQEQLLREHYQKKFKNSTYSRSSVDVLYTFANCSGLDLIFGL 188
 DB 122 SERVSADVLRLQWMPFQELLLREYQREKFNSTYSRSSVDMLYSPAKCSRDLIFGL 181
 QY 189 NALRTADLQWSSNAQILLDYCSSKGYNISWELGNEPNSFLKKADIFINSGQGEDVYE 248
 DB 182 NALRTPDRLRWSSNAQILLNLCSSKGYNISWELGNEPNSFWKKAQISIDGLQGEDVYE 241
 QY 249 LHKLRKSTFPKNAKLYGPDVGQPRRKTAKMLKSPKAGGEVIDSYTMHHYLLNGRTATRE 308
 DB 242 LHKLLQKSAFQNAKLYGPDIGQPRKTYKLRSLFKAGGEVIDSLTMHHYLLNGRVATKE 301
 QY 309 DFLNPVDLIFISSYQKVFQVVESTRPGKRWLGETSAYGGAPLSDTPAAGFMWLDK 368
 DB 302 DFLSSDVLDTFLISVQKILKTKEMTPGKRWLGETSAYGGAPLSDTPAAGFMWLDK 361
 QY 369 LGLSARMGIEVVMRQVFFGAGNYHLVDENFPLPYWLSLFLKLVGTRKYLMAVSQSKR 428
 DB 362 LGLSAQLGIEVVMRQVFFGAGNYHLVDENFPLPYWLSLFLKLVGTRKYLMAVSQSKR 421
 QY 429 RKLRYLHCTNDNRYKEGDLTLYAHLNHTKYLRLPYFPNSKQVDKYLRLPGPGL 488
 DB 422 SKLRVYLHCTNVYHRRYREGDLTLVNLNHTKYLKLPMPFSPRPVDKYLRLKPGSGDL 481
 QY 489 LSKSVQNLGLTLKQVDDQTLPLMEKPLRPSSSLGLPAFYSFVYIRNAKVAACI 543
 DB 482 LSKSVQNLGLTLKQVDDQTLPLMEKPLRPSSSLGLPAFYSFVYIRNAKVAACI 536

RESULT 7
 Q9QZF8 PRELIMINARY; PRT; 536 AA.
 AC Q9QZF8;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hepatanae.
 GN Name=Hep;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22194309; PubMed=12077130; DOI=10.1074/jbc.M203282200;
 RA Podjma-Inoue K.A., Yokoe H., Sakaguchi K., Ikuta M., Yanagishita M.;
 RT "Characterization of heparanase from a rat parathyroid cell line."
 RL J. Biol. Chem. 277:32459-32465(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Podjma K.A., Yokoe H., Sakaguchi K., Ikuta M., Yanagishita M.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF184967; AAF04563.1; -
 DR InterPro; IPR005199; Glyco_hydro_79N.
 DR Pfam; PF03662; Glyco_hydro_79n; 1.
 SO SEQUENCE 536 AA; 60568 MW; 6208B1FDEE28421 CRC64;

Query Match 74.7%; Score 2123; DB 2; Length 536;
 Best Local Similarity 75.7%; Pred. No. 9.5e-151;
 Matches 405; Conservative 51; Mismatches 79; Indels 0; Gaps 0;

QY 9 LPPRLMLLLGLPLGSPGALPRPAQADVDLDPFQGEPLHLVSPSLSTVIANLATD 68
 DB 2 LRPILLMLWGRGLALTGTPAGTAPTKOVVDLEFRTKLFQSVSPSLSTITIASLATD 61
 QY 69 PRFLILGSPRLRLTARGLSPAYLRFGGTKTDPLIFDPKKESTFEERSYWSQVNDICK 128
 DB 62 PRFLIFLGSPLRLALARGSPAYLRFGGTKTDPLIFDPKKESTFEERSYWSQVNDICK 121
 QY 129 YGSIIPDVEEKLRLMEPYQEQLLREHYQKKFKNSTYSRSSVDVLYTFANCSGLDLIFGL 188
 DB 122 SERVSADVLRLQWMPFQELLLREYQREKFNSTYSRSSVDMLYSPAKCSRDLIFGL 181
 QY 189 NALRTADLQWSSNAQILLDYCSSKGYNISWELGNEPNSFLKKADIFINSGQGEDVYE 248
 DB 182 NALRTPDRLRWSSNAQILLNLCSSKGYNISWELGNEPNSFWKKAQISIDGLQGEDVYE 241
 QY 249 LHKLRKSTFPKNAKLYGPDVGQPRRKTAKMLKSPKAGGEVIDSYTMHHYLLNGRTATRE 308
 DB 242 LHKLLQKSAFQNAKLYGPDIGQPRKTYKLRSLFKAGGEVIDSLTMHHYLLNGRVATKE 301
 QY 309 DFLNPVDLIFISSYQKVFQVVESTRPGKRWLGETSAYGGAPLSDTPAAGFMWLDK 368
 DB 302 DFLSSDVLDTFLISVQKILKTKEMTPGKRWLGETSAYGGAPLSDTPAAGFMWLDK 361
 QY 369 LGLSARMGIEVVMRQVFFGAGNYHLVDENFPLPYWLSLFLKLVGTRKYLMAVSQSKR 428
 DB 362 LGLSAQLGIEVVMRQVFFGAGNYHLVDENFPLPYWLSLFLKLVGTRKYLMAVSQSKR 421
 QY 429 RKLRYLHCTNDNRYKEGDLTLYAHLNHTKYLRLPYFPNSKQVDKYLRLPGPGL 488
 DB 422 SKLRVYLHCTNVYHRRYREGDLTLVNLNHTKYLKLPMPFSPRPVDKYLRLKPGSGDL 481
 QY 489 LSKSVQNLGLTLKQVDDQTLPLMEKPLRPSSSLGLPAFYSFVYIRNAKVAACI 543
 DB 482 LSKSVQNLGLTLKQVDDQTLPLMEKPLRPSSSLGLPAFYSFVYIRNAKVAACI 536

RESULT 8
 Q9QYK5 PRELIMINARY; PRT; 523 AA.
 AC Q9QYK5;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hepatanae.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21369599; PubMed=11387326; DOI=10.1074/jbc.M102462200;
 RA Goldsmith O., Zcharia E., Aingorn H., Guarta-Rangini Z., Azmon R.,
 RA Michael I., Becker I., Mitrani E., Vlodavsky I.;
 RT "Expression pattern and secretion of human and chicken heparanase are
 determined by their signal peptide sequence."
 RL J. Biol. Chem. 276:29178-29187(2001).
 DR EMBL; AY037007; AAK82648.1; -
 DR Pfam; PF03662; Glyco_hydro_79n; 1.
 SO SEQUENCE 523 AA; 58386 MW; 8EB0B7B18C9BF881 CRC64;

Query Match 57.9%; Score 1645.5; DB 2; Length 523;
 Best Local Similarity 60.2%; Pred. No. 6.8e-115;

Matches 320; Conservative 87; Mismatches 114; Indels 11; Gaps 3;

```
QY 13 IMLLLGPIGSPGLPRPAQOVVDIDFTQEPHLVSPSLVTIDANLATDPRFL 72
D 2 LVLLLVLLLVLP-----RRVAFELQGLRREPIGAVSPAFSLTLDASLARDRFV 52
QY 73 ILLGPKRTTLARGLSPAYLRFQGTDPFLIPDPKKESTFEERSTWQOVNODICKYGI 132
D 53 ALIRHFKHTLASGSPGLRFGCTDPFLIPNPKMDSTWEEKVSEFOA-KDYCEAMPS 111
QY 133 PPDVEKRLRWEPYOBQLLRHYOKKRNSTYSRSSVDVLYTFPANGSGDLIFGLNAL 192
D 112 FAVPEKLTQMPLEKRLHAEHSWKKKNTTITRSTDLIATPASSGPRLVGNAAL 171
QY 193 PPAIDQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKADIFINSQIGEDYIOLHKL 252
D 172 RAGGIQMDSSNAKQLIGYCAQSYNISWELGNEPNSFRKSGICIDFQGRFVHLROL 231
QY 253 L-RKSTFPAKLYGPDVQPPRKTAKMLKSFLLKAGEVIDSVTWHNYLLNGRTATREDFL 311
D 232 LSGHPLRYHAEVLGIDVQGPRTKHQHLRSEFMKSGKALDSVTWHNYVNGRATREDFL 291
QY 312 NPVDLDFISSVQKVFQVVESTPRGKVMGETSSAYGAGAPLSTPFAAGFMWLDKGL 371
D 292 SPEVLDFSPATAIHDVLTGIVENTVGGKVMIGETGSAIGGAPQLSNTTYAAGFMWLDKGL 351
QY 372 SARGIEVWMOVFQFGAGNHLVDENFDPLPDYMLSLFPAKLVGTVMASVQSGKRL 431
D 352 AARGIDVWMOVQSFQSGYHLVDAGFKPLPDYMLSLYRLVGTVMASVQSGKRL 411
QY 432 RVLVHCTNTDNPKEGDLTLVYAINLHNTKYRLRPPSNQOVNODICKYLRPGHGLSK 491
D 412 RVLVHCTNPRPKREDVTLPLNLSNTQSLQPLKQMSKSVQVYLLPFGKDSILSR 471
QY 492 SYQNGTLTKMVDQTLPLMEKPLRPGSSLGHPAFYSFFYIRNAKVAAC 543
D 472 EVQNGELQLQWVDETLPLHEMALAPGSLTGLPARYGFFYIRNAKVAAC 523
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RESULT 9

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Q9HB37 PRELIMINARY; PRT; 592 AA.
AC Q9HB37;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
DB Hepatanase-like protein HPa2c.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20483645; PubMed=11027606; DOI=10.1006/dbrc.2000.3586;
RA McKenzie E., Tyson K., Stamps A.,
RA Hircock M., Patel S., Barry R., Stuberfield C., Terrett J.,
RT "Cloning and expression profiling of Hpa2, a novel mammalian
RL heparanase family member."
RN Biochem. Biophys. Res. Commun. 276:1170-1177 (2000).
RP SEQUENCE FROM N.A.
RA McKenzie E.A., Tyson K., Stamps A.,
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282887; AAC23423.1;
DR GO; GO:0005622; C:intracellular; TMS.
DR GO; GO:0030305; F:heparanase activity; TMS.
DR InterPro; IPR005199; Glyco_hydro_79n;
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 592 AA; 66580 MW; 95C384AD9A74258E CRC64;
```

Query Match

Best Local Similarity 40.6%; Score 1154.5; DB 2; Length 592;
Matches 250; Conservative 82; Mismatches 189; Indels 53; Gaps 9;

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QY 20 PLGSPSPGL-----PRPA-----QAQVVDLDFTQEPHLVSPS 55
D 18 PPAIAFGALYALALHLHLSQAGDRRLPLVDAAAGKKTILLVSTKNPVRNVEN 77
QY 56 FLSVTIDANLATDPRFLILLSPKRLTARGLSPAYLRFQGTDPFLIF----DPKKEST 111
D 78 FLSLDLDSIIHD-GMLDFLSSKRLVTLARGLSPAYLRFQGTDPFLQFQNLNPAKSRG 136
QY 112 FEERSWQOVNODI-----CKYGSIPPDVEKRLRWEPYOBQL-LRREHYOK 158
D 137 GGPEDVYIAKNVEDIIVRSVDVALDKQKCKIAQ-HPDVMLEQREKAAQMHVLKQFSN 195
QY 159 KFKNSTYRSSVDVLYTFPANGSGDLIFGLNALLRITADQWSSNAQLLDYCSSKGYNI 218
D 196 TYSNLITANSBLDKLNFADSCSGLHIFALNARRPNNSWSSSALSLKTSASKYNI 255
QY 219 SWELGNEPNSFLKADIFINGSQIGEDYIOLHKLRLK-STFPAKLYGPDVQPPRKTA 277
D 256 SWELGNEPNNYRIMHGAVVQSGQIGKDYIQKSLQPIPIYRSASLYGPNIRPKNYIA 315
QY 278 MLKSFLLKAGEVIDSVTWHNYLLNGRTATREDFLNPVDLDFISSVQKVFQVVESTPRGK 337
D 316 LIDGFMKAVGSTVDAYWQHCHYIDGRVVMDFLTKRLDLTSDQIRKIQKVMVYTFGK 375
QY 338 KVMIGETSSAYGAGAPLSTPFAAGFMWLDKGLSARGIEVWMOVFQFGAGNHLVDEN 397
D 376 KIMLEGVTTASAGCTNNLSDSAAGFMWLDKGLSARGIEVWMOVFQFGAGNHLVDEN 435
QY 398 FDLPLPYMLSLFPAKLVGTVMASVQSGKRL-----KLRYLHCTNTDNPKEG 448
D 436 FNLPLPYMLSLYKRLIGPKVLAHVAGIQRKPRGRVIRDKRLRYAACHNHNHNVRG 495
QY 449 DLTVAINLHNTKYRLRPPSNQOVNODICKYLRPGHGLSKSVQNGTLTKMVDQTL 508
D 496 SITLFTINLHRSRKIKLAGTRIDLVYQYLLQYGGGLSKSVQNGTLTKMVDQTL 555
QY 509 PPLMEKPLRPGSSLGHPAFYSFFYIRNAKVAAC 542
D 556 PELKRPPLRAGRTLVIPVTWGFVYVKNVNALAC 589
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RESULT 10

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Q8WMQ2 PRELIMINARY; PRT; 592 AA.
AC Q8WMQ2;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)
DB Hepatanase 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20483645; PubMed=11027606; DOI=10.1006/dbrc.2000.3586;
RA McKenzie E., Tyson K., Stamps A.,
RA Hircock M., Patel S., Barry R., Stuberfield C., Terrett J.,
RT "Cloning and expression profiling of Hpa2, a novel mammalian
RL heparanase family member."
RN Biochem. Biophys. Res. Commun. 276:1170-1177 (2000).
RP SEQUENCE FROM N.A.
RA McKenzie E.A., Tyson K., Stamps A.,
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282887; AAC23423.1;
DR GO; GO:0005622; C:intracellular; TMS.
DR GO; GO:0030305; F:heparanase activity; TMS.
DR InterPro; IPR005199; Glyco_hydro_79n;
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 592 AA; 66520 MW; 947841F8ACD558B CRC64;
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Query Match

Best Local Similarity 40.3%; Score 1146.5; DB 2; Length 592;
Matches 249; Conservative 82; Mismatches 190; Indels 53; Gaps 9;

[illegible]

Db 6 AFPEMSSNSRPPACIARGLAYIALLLHLSLSQAGRRRLPVDNRAAGLAKEXTIILLDV 65

Qy 4 FTQEBLHVSPSFLSVTTIDANLATDPREFLLIGSPKLTTLARGLSPAYLRFQGTDTPLI 103

Db 66 STKNPVRTVNEFNLSIQDPISIIHD-GWLDFLSSKRLVTTLARGLSPALRFQGTDTPLQ 124

Qy 104 F----DPKKESTFEERSYQSQVNODI-----CKGSIIPRVEEKLREMYQ 147

Db 125 FQNTLRNPKSRGSGPPDYLLKNYEDDIYRSDVALDKQKCKIAQ-HPDVMELEOREKAAQ 183

Qy 148 EQL-LIREHYOKKFKFNSTYSRSSVDVLTYPANCSGLDIPGLNALRTADIQMNSNAOL 206

Db 184 MHLVLKQKQFNTSYNSLILTRSRISDLKLYNSADCSGLHIFALNALRRPNPNSMSSALS 243

Qy 207 LLDYCSSKGYNISWELGNEPNSFLKKADIFINGSQLEGDYIQLHKLLRK-STFKNAKLYG 265

Db 244 LKKSASAKKYNISWELGNEPNNYRTMHGRAVYNGSQLGKDYIQLKSLIPRIYSPALSYG 303

Qy 266 PDVGQPRKTKAMLKSPFKAGGEYIDSTYHHYILNGRTATREDPLANDVDIFISSQK 325

Db 304 PNIGPRKQVIALLDGFMKAVGASTVDATWQHCYIDGRVVKVMPFLKTRLLDTLSQIRK 363

Qy 326 VEOYVESRPPKKWMLGFTSSAYSAGCAVLSDTFAAGRWMLDKGLSARMGIEVMRQVF 385

Db 364 IQKVNTTTPGKKIYLBGVVTTSSAGGTNNSDSTAAGFLMTLNTGLMANOGIDVIRISF 423

Qy 386 FGAGNYHLVDENFDPLPDYWLSSLFKLVGTRKVLMAVSQSKRR-----KLRVYLH 436

Db 424 FDHGVNHLVDQNFNPPLPDYWLSSLKYRLIGKVLAVNHAAGLQKRPGRVIRDKLRIYAH 483

Qy 437 CTNTDNPYKGGDLTLVAINLHNTKYRLRPPSNKQVDKYLRPLGPHGLSKS 492

Db 484 CTNNHNNHYVAGSITLFIINLHRSRKIKLAGTLRDKLVLHGYLLQPYQGEGLKSKT 539

RESULT 12

Q9HB38 PRELIMINARY; PRT; 534 AA.

AC Q9HB38; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DS Hepatanae-like protein HPA2b.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN RN SEQUENCE FROM N.A.

RP MEDLINE=20483465, PubMed=11027606, DOI=10.1006/jbrc.2000.3586;

RA McKenzie E., Tyson K., Stamps A., Smith P., Turner P., Barry R.,

RA Hittcock M., Patel S., Barry E., Stubberfield C., Terrett J., Page M.,

RT "Cloning and expression profiling of Hpa2b, a novel mammalian

RL hepatanae family member."

RL Biochem. Biophys. Res. Commun. 276:1170-1177(2000).

RN RN SEQUENCE FROM N.A.

RP McKenzie E.A., Tyson K., Stamps A.;

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF282886; AAG34422.1; -

DR InterPro; IPR005199; Glyco_hydro_79N.

DR Pfam; PF03662; Glyco_hydro_79n; 1.

DR SEQUENCE 534 AA; 60063 MW; C3DE5F90CB338C4 CRC64;

Query Match 33.0%; Score 936.5; DB 2; Length 534;

Best Local Similarity 37.8%; Pred. NO. 1.3e-61;

Matches 217; Conservative 78; Mismatches 168; Indels 111; Gaps 12

Qy 20 PLGIPSPAL-----PRPA-----QAQDVLDFFTOEPLHLVSPS 55

Db 18 PPACIARGLAYIALLLHLSLSQAGRRRLPVDNRAAGLAKEXTIILLDVSTKNPVRTVNE 77

Qy 56 FLAVTIDANLATDPREFLLIGSPKLTTLARGLSPAYLRFQGTDTPLI----DPKKEST 111

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Db 78 FLSTQDPSIIHD-GWLDFFLSKRLVTIARGLSPAFYRFGGKRTDFLOFQULRNPASRG 136
Qy 112 FEERSYMSQVNOI-----CKYGIIPDVEEKLRLWPYQOL-LTREHYOK 158
Db 137 GPGPDYIHKYEDDIIVRSVALDKOKGCKIAQ-HPDVMLELQREKAQMHLVILKEGF-- 133
Qy 159 KFKSTYSRSSVDVLYTFPANCSGLDLIFGLNALRTADLQWSSNAQLLDYCSSKGYNI 218
Db 194 ---SNVYS-----NLIT----- 202
Qy 219 SWEIGNEPNSFLKADIFINGSQIGEDYIOLHKLK-STEKNAKLYGPDVGPRRKTKA 277
Db 203 -----TEBNNYRTMHGRAVNGSOLGKDYIOLKSLQIRIYSRASILGPIGPRKXVIA 257
Qy 278 MLKSLFKAAGEVIDSYTHHYYLNGRTATREDFLNDPVDLFISSVQKVFQVESTPCK 337
Db 258 ILDSFPMVAGSYDAVYWHQCHYIDGRVYKVMDFLKRLLDITLSDOIIRKIQKVNVYTPCK 317
Qy 338 KWIIGETSSAYGGAPLLSDTFAAGFMWLDKLGLSARMGIEVYMRQVFFGAGNYHLVDEN 397
Db 318 KIWLEGVVITTSAGGTNNLSDSYAAFLMNTLGLANOGIDVYIRHSFPDHGYNHLVDON 377
Qy 398 FDPFLPYWLSLFRKLVGTQVLMASVQSGRR-----KLRYLHCTNTDNPRYKMG 448
Db 378 FNPFLPYWLSLFRKLVGTQVLMASVQSGRR-----KLRYLHCTNTDNPRYKMG 437
Qy 449 DLTLYAINHNVTYKRLRPPFSNKQVQYLLRPLGPHGLSKSVQNLGLTKMYDDOTL 508
Db 438 SILFTFINLHRSRKKIKLAGTLRDLKVHGYLLQPYGEBLKSQVQNLGQPLVMWDDGTL 497
Qy 509 PLMEKPLRPGSLGLPAPSYSPFYIRAKVAAC 542
Db 498 PELKPRPLRAGRTLVYPVTMGFFVKVNNALAC 531

```

RESULT 13

Q9HB39

ID Q9HB39 PRELIMINARY; PRT; 480 AA.

```

AC 09HB39;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Heparanase-like protein HPA2a.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20483645; PubMed=11027606; DOI=10.1006/jbrc.2000.3586;
RA McKenzia E.A., Tyson K., Stamps A., Smith P., Turner P., Barry K.,
RA Hitecock M., Patel S., Barry E., Stuberfield C., Terrett J., Page M.;
RT "Cloning and expression profiling of Hpa2, a novel mammalian
RT Heparanase family member."
RL Biochem. Biophys. Res. Commun. 276:1170-1177(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA McKenzia E.A., Tyson K., Stamps A.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282885; AAC3421.1; -.
DR JGI; J0506; J0506.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 480 AA; 53900 MW; F75F89F67AC1PF83 CRC64;

```

Query Match

Best Local Similarity 31.6%; Score 897.5; DB 2; Length 480;
Matches 202; Conservative 74; Mismatches 146; Indels 139; Gaps 9;

Qy 20 PLGSPGAI-----PRPA-----OAOVVDVDFPTQSPHLVPS 55
Db 18 PPAALPAGALYALLLHLSTLSQAGRRPLPVDRAAGLKEKTLILLDYSTKQPVRTVEN 77

```

Qy 56 FLSTVITDANLADPRFLILSSPKLRTIARGLSPAYIRFGGKTKDPIF-----DPKKEST 111
Db 78 FLSTQDPSIIHD-GWLDFFLSKRLVTIARGLSPAFYRFGGKRTDFLOFQULRNPASRG- 135
Qy 112 FEERSYMSQVNOI-----CKYGIIPDVEEKLRLWPYQOL-LTREHYOKKFKSTYSRSSVD 171
Db 136 -----GGGPD-----YLLKNY----- 148
Qy 172 VLYTPANCGLDIFGLNALRTADLQWSSNAQLLDYCSSKGYNI-SWEIGNEPNSFLK 231
Db 149 -----DEPNNYRT 156
Qy 232 KADIFINGSQIGEDYIOLHKLK-STEKNAKLYGPDVGPRRKTKAKMLKSLFKAAGEVY 290
Db 157 MGRGAVNGSOLGKDYIOLKSLQIRIYSRASILGPIGPRKXVIALLDGFMKAVGASTV 216
Qy 291 DSYTHHYYLNGRTATREDFLNDPVDLFISSVQKVFQVESTPCKKWLGETSSAYGG 350
Db 217 DAVYWHQCHYIDGRVYKVMDFLKRLLDITLSDOIIRKIQKVNVYTPCKKIIMLBSGVITTSAG 276
Qy 351 GAPLLSDTFAAGFMWLDKLGLSARMGIEVYMRQVFFGAGNYHLVDENPPLPDYWLSTLF 410
Db 277 GTNNLSDSYAAFLMNTLGLANOGIDVYIRHSFPDHGYNHLVDONFNPFLDYWLSTLY 336
Qy 411 KKLVTQVLMASVQSGRR-----KLRYLHCTNTDNPRYKMGDTLYAINLHNVT 461
Db 337 KRLIGPVLAHVAGLQKRPGRVIRDKLRIYAHCTNHNNHYRGSTITPLINLHRS 396
Qy 462 KYLRLPFPFSNKQVQYLLRPLGPHGLSKSVQNLGLTKMYDDOTLPLMEKPLRPGSS 521
Db 397 KKKIAGTLRDLKVHGYLLQPYGEBLKSQVQNLGQPLVMWDDGTLPELKRPLRAGRT 456
Qy 522 LGLPAPSYSPFYIRAKVAAC 542
Db 457 LVLPVTMGFFVKVNNALAC 477

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RESULT 14

O8T108

ID O8T108 PRELIMINARY; PRT; 515 AA.

```

AC O8T108;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Heparanase-like protein.
GN Name=Bmbp2; (Silk moth).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=p50; TISSUE=Posterior silk gland;
RA Koike Y., Mita K., Suzuki M.G., Maeda S., Abe H., Osoegawa K.,
RA deJong P.J., Shimada T.;
RT "Genomic sequence of a 320-kb segment of the Z chromosome of Bombyx
RT mori containing a kettin ortholog."
RL Mol. Genet. Genomics 269:137-149(2003).
DR EMBL; AB079860; BAB85191.1; -.
DR EMBL; AB090307; BAC10612.1; -.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 515 AA; 59769 MW; FB810AB6EDDADB CRC64;

```

Query Match

Best Local Similarity 24.5%; Score 696; DB 2; Length 515;
Matches 189; Conservative 83; Mismatches 182; Indels 74; Gaps 18;

Qy 46 QEPHLVSPSELSVTIDANLADPRFLILSSPKLRTIARGLSPAYIRFGGKTKDPIFD 105
Db 42 QEDIKLISDFISFGID-TIETENYKRYNSDTRLELAALSPARLRLRGITMSERLIF- 99

QY 106 PKSESTFEERSYQWQVNOQDICKYGISIPDVEKLEMPYQBOQLLREHYOKKFKNSTY 165
DB 100 -SKENI-----PISCHNCSYKSYKSLCQ--LIEKPC-----KHKKKFLPFITM 140
QY 166 SRSSVDVLYTFANCSGLDLIFGLNALRTADLQWNSNAQLLDYCSSKGYNISWELGNE 225
DB 141 TGNENWQINDPFCRKTNLKLFLSLNMLRD-NHGMMEKARBELIEFSKHQVADIDQLGNE 199
QY 226 PMSFLKADIFINGSQLEDYIQLHKLKRSFTFNKAKLYGPDVGP---RRTATMLKSF 282
DB 200 PMSFHVNESVTPOILAKDPEKRLKLNHNGYRSLVGPDTTPRQPHRPECLKYLIEF 259
QY 283 LKAGEVIDSVTHHYLYNGRTATREDFLNPDVLIFISSVQKVQVVESTPCKV--W 340
DB 260 LANGSHYINVRSMHYYLNSKTAKEDEFWNPETPOL--RQIETMQNQTCKYKNIEM 316
QY 341 LGETSSAYGGAPLLSDTFAAGFMWLDKLGLSARNGIEVNRQVFFGAGNYHLDENPD 400
DB 317 LSETSSYGGAGPLSNTYAGSPMLWIDKLGLSAKYNISFVIRQSPFG--GYSLVDENLKP 375
QY 401 LPDYLSLFLKLVGTGYLMAVQGSKRKRLRVYLHCTNTDNPRYKE--GDILTYAIN-- 456
DB 376 LPDWMISVLYKKLVGNKYL--QVQNCGRFQRLYHCTNR--KYTNDITSATLYGVNDE 430
QY 457 -----LHN-----VTKYRLPYPPFSNKQVDKYLLRPLGPHGLSKSVOLNGLTL 500
DB 431 MAKAPFLNGTALHGDLDLIHEYI-ISAPSNRK-----SKTIILNGMPL 474
QY 501 KMWDDQTLPLMEKPLRPSSLSGLPAFSYSPFVINNAKVAAC 542
DB 475 YY--ESNLHNLRLPNHRYGRVYSLPPYSIGFWVIKTSITVC 514

RESULT 15

Q9SDA1 PRELIMINARY; PRT; 521 AA.
ID Q9SDA1 AC Q9SDA1; 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Hypothetical protein F13G24.30.
GN Name=F13G24.30;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustosida II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Beyan M., Van Der Schueren J., Chuang Y.J., Voet M., Robben J.,
RA Voleckaert G., Bancroft I., Mewes H.W., Lemcke K., Mayer K.F.X.,
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DB EMBL; AL133421; CAB62595.1; --
DR PIR; T45608; T45608.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF03662; Glyco_hydro_79n_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hypothetical protein.
KW SEQUENCE 521 AA; 57831 MW; 07D8664AAB305CC2 CRC64;

Query Match 14.6%; Score 416; DB 2; Length 521;
Best Local Similarity 29.2%; Pred. No. 1.6e-22;
Matches 154; Conservative 68; Mismatches 184; Indels 122; Gaps 24;

QY 75 LGSPKLTURLANGSLPAYRFGSTKTDPLIFDPKKESTFEERSYQWQVNOQDICKYGISIP 134
DB 55 LTRPLTLRAIKAFKFLIRIGSLDQVIVDGNLKT-----PCR----- 94

QY 135 DVEEKLRLMPYQBOQLLREHYOKKFKNS---TYSRSSV-----DLYTFANCSGLDLIF 186
DB 95 -----PQCK-----NSGLFGSSKGLHKKRDELNSFLTATCAVTF 132
QY 187 GLNALRTADLQ-----WNSSNAQLLDYCSSKGYNI-SWELGNEPNSFLKADIFIN 238
DB 133 GLNMLRGHKLRGKAMGAMDHINTQDPLANTVSKGYIDSMERGNEISG--SGVGASVS 190
QY 239 GSQGEDYIQLHKLKRSFTFNKAKLYGPDVGP-----RRTATMLKSFLLAGEVIDSV 293
DB 191 AELYGKDLIVLKDVYINK--VYNSWLHKLIVAPGFGYEQQWYTKLLET--SGBSVDVV 246
QY 294 TWHHYLYNGRT--ATREDFLNPDVLIFISSVQKV-----QVSESTRGKKWLGETSSA 347
DB 247 THHLYNLSGNDPALVKKIMPS-----YLSQVSKTFKQVNTIQHGHWAPWVGSIGA 302
QY 348 YGGAPLLSDTFAAGFMWLDKLGLSARNGIEVNRQVFFGAGNYHLDENPDLPDYWL 406
DB 303 YNSGGRHVSDFIDSFWYLDQLGMSARHNTKYVCGQLVG--GFYGLLEKGFVPRPDYYS 361
QY 407 SLFLKLVGTGYLMAVQGSKRKRLRVYLHCTNTDNPRYKEGDLTYAINLHNTKYL-- 464
DB 362 ALLMHRLMKGVLAVQTDGPP--QLRYVAHCSK-----GRAGYTLILINLSNOSDFTVS 413
QY 465 -----RLPYPPFS---NKQVDKYLLR---LGPHG--LISKVQL 495
DB 414 VSNGINVVLNAESRKKSLLTLKRPFSWTSKASDGYLNREETHLTPENGVLSKTIWVL 473
QY 496 NGLTLKMWDDQTLPLMEKPLRP--GSLGLPAFSYSPFVINNAKVAAC 542
DB 474 NKSILKPTATGDIPSL--EPVLRSVNSPLNVLPLMSFVLNPDASAC 520

Search completed: February 28, 2005, 06:08:39
Job time : 184 secs

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CC conditions such as wound healing, angiogenesis, restenosis,
 CC atherosclerosis, inflammation, neurodegenerative diseases, and viral
 CC infections. Mammalian heparanase can be used to neutralize plasma
 CC heparin, and anti-heparanase antibodies may be applied for
 CC immunodetection and diagnosis of micrometastases, autoimmune lesions, and
 CC renal failure in biopsy specimens, plasma samples, and body fluids. The
 CC present sequence represents human heparanase
 CC
 SQ Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 2; Length 543;
 Best Local Similarity 100.0%; Pred. No. 2.5e-273;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVDVLPFQEPHLVSPFLSYT 60
DB 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVDVLPFQEPHLVSPFLSYT 60
QY 61 IDANLATDRPFLILGSPKLTARGLSPAYLRFQGTKTDFLPDPKKESTFEERSYMQS 120
DB 61 IDANLATDRPFLILGSPKLTARGLSPAYLRFQGTKTDFLPDPKKESTFEERSYMQS 120
QY 121 QVNODICKGSIIPVVEEKLRLMEPYQEQLLREHYOKKFKNSTYSRSVDVLYTFANCS 180
DB 121 QVNODICKGSIIPVVEEKLRLMEPYQEQLLREHYOKKFKNSTYSRSVDVLYTFANCS 180
QY 181 GDLIFGALNALTADLQWNSNAQLLDYCSSKGYNISWELGNPNPFLKKADIFINGS 240
DB 181 GDLIFGALNALTADLQWNSNAQLLDYCSSKGYNISWELGNPNPFLKKADIFINGS 240
QY 241 QUGEDYIQLHKLIRKSTFKNALYGPVVGQPRKTKAKMLKSFLLKAGGEVIDSVTWHYYL 300
DB 241 QUGEDYIQLHKLIRKSTFKNALYGPVVGQPRKTKAKMLKSFLLKAGGEVIDSVTWHYYL 300
QY 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTRGKKVWLGETSAYGGAPLLSDTFA 360
DB 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTRGKKVWLGETSAYGGAPLLSDTFA 360
QY 361 AGFWMLDLKGLSARNGIEVVMKQVFFGAGNHLVDENFDPLPDYWLSLFFKLAVGTVM 420
DB 361 AGFWMLDLKGLSARNGIEVVMKQVFFGAGNHLVDENFDPLPDYWLSLFFKLAVGTVM 420
QY 421 ASVQSKRKRLRVYHCTNTNPRYKEDLTLYAINLHNTKYRLPYPSNKQVDXYLL 480
DB 421 ASVQSKRKRLRVYHCTNTNPRYKEDLTLYAINLHNTKYRLPYPSNKQVDXYLL 480
QY 481 RPLGPHGLSKSVQNLGLTLKAVDQTLPLMEKPLRPGSSLGHPASYSFFVIRNAKVA 540
DB 481 RPLGPHGLSKSVQNLGLTLKAVDQTLPLMEKPLRPGSSLGHPASYSFFVIRNAKVA 540
QY 541 ACI 543
DB 541 ACI 543

```

RESULT 2
 ID AAY57590
 AAY57590 standard; protein; 543 AA.

DT 02-MAR-2000 (first entry)

DE Human heparanase.
 XX Human, heparanase; hpa; genetic modification; expression; anticancer;
 KM angiogenesis; anti-angiogenic; antiproliferative; antiviral; antitumor;
 KM anti-atherosclerotic; anti-inflammatory; antineurodegeneration;
 KM heparan sulphate; heparin-binding factor; tumour angiogenesis;
 KM metastasis; wound healing; restenosis; atherosclerosis; inflammation;
 KM neurodegeneration; viral infection; cystic fibrosis; cancer; diagnosis;
 KM micrometastasis; autoimmune lesion; kidney failure.
 XX

OS Homo sapiens.
 XX
 XX WO957244-A1.
 XX
 XX 11-NOV-1999.
 PD
 XX
 XX 29-APR-1999; 99WO-US009256.
 PF
 XX
 XX 01-MAY-1998; 98US-00071618.
 PR
 XX 02-MAR-1999; 99US-00260038.
 XX
 PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
 PA (FRIE/) FRIEDMAN M M.
 XX
 PI Ben-Artzi H, Ayal-Herskovitz M, Yacoby-Zeevi O, Pecker I;
 PI Peleg Y, Shlom Y;
 DR N-PSDB; AAZ39195.
 DR WPI; 2000-062144/05.
 PT Engineered cells that express recombinant heparanase, useful
 PT therapeutically, e.g. for treating angiogenesis and to screen for
 PT specific inhibitors, potential anticancer agents.
 PS
 XX
 XX Claim 3; Page 107-109; 118pp; English.

The present invention describes genetically modified cells (A) containing a polynucleotide (I) that encodes a polypeptide with heparanase activity, and express recombinant heparanase (II). Heparanase cleaves heparan sulphate (HS) at specific intrachain sites, resulting in release of heparin-binding growth factors, enzymes and proteins that are sequestered by HS in basement membranes, extracellular matrix or cell surfaces. It may also be implicated in tumour angiogenesis and metastases. (II) is potentially useful in wound healing and for treating angiogenesis, restenosis, atherosclerosis, inflammation, neurodegeneration, viral infection and cystic fibrosis. It can also be used to neutralise heparin (an alternative to protamine) and to screen for specific inhibitors (potentially useful for treating cancer and metastases). Antibodies raised against (II) are used for immunodetection and diagnosis of micrometastases, autoimmune lesions and kidney failure. (A) provide (II) in large quantities, in a form that is homogeneously processed and activated/neutralised by a dedicated protease. The present sequence represents human heparanase

SQ Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 3; Length 543;
 Best Local Similarity 100.0%; Pred. No. 2.5e-273;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVDVLPFQEPHLVSPFLSYT 60
DB 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVDVLPFQEPHLVSPFLSYT 60
QY 61 IDANLATDRPFLILGSPKLTARGLSPAYLRFQGTKTDFLPDPKKESTFEERSYMQS 120
DB 61 IDANLATDRPFLILGSPKLTARGLSPAYLRFQGTKTDFLPDPKKESTFEERSYMQS 120
QY 121 QVNODICKGSIIPVVEEKLRLMEPYQEQLLREHYOKKFKNSTYSRSVDVLYTFANCS 180
DB 121 QVNODICKGSIIPVVEEKLRLMEPYQEQLLREHYOKKFKNSTYSRSVDVLYTFANCS 180
QY 181 GDLIFGALNALTADLQWNSNAQLLDYCSSKGYNISWELGNPNPFLKKADIFINGS 240
DB 181 GDLIFGALNALTADLQWNSNAQLLDYCSSKGYNISWELGNPNPFLKKADIFINGS 240
QY 241 QUGEDYIQLHKLIRKSTFKNALYGPVVGQPRKTKAKMLKSFLLKAGGEVIDSVTWHYYL 300
DB 241 QUGEDYIQLHKLIRKSTFKNALYGPVVGQPRKTKAKMLKSFLLKAGGEVIDSVTWHYYL 300
QY 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTRGKKVWLGETSAYGGAPLLSDTFA 360
DB 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTRGKKVWLGETSAYGGAPLLSDTFA 360

```

QY 361 AGFWMLDLGLGSARWGIEVWNRQVFGAGNYHLVDENFDPLPDYWLSTLFFKKLVGTXYLM 420
|||
DB 361 AGFWMLDLGLGSARWGIEVWNRQVFGAGNYHLVDENFDPLPDYWLSTLFFKKLVGTXYLM 420
QY 421 ASVQGSKRKRKLRYVYLHCTNTDNPARYKEGDLTLVAIINLHNVTKYLRLPYFPSNKOVDXYLL 480
421 ASVQGSKRKRKLRYVYLHCTNTDNPARYKEGDLTLVAIINLHNVTKYLRLPYFPSNKOVDXYLL 480
DB 421 ASVQGSKRKRKLRYVYLHCTNTDNPARYKEGDLTLVAIINLHNVTKYLRLPYFPSNKOVDXYLL 480
QY 481 RPLGPHGLLSKSVQVNLGLTLKAVDDQTLPLMEKPLRGGSLGLPAFYSFFVIRNAKVA 540
481 RPLGPHGLLSKSVQVNLGLTLKAVDDQTLPLMEKPLRGGSLGLPAFYSFFVIRNAKVA 540
DB 481 RPLGPHGLLSKSVQVNLGLTLKAVDDQTLPLMEKPLRGGSLGLPAFYSFFVIRNAKVA 540
QY 541 ACI 543
|||
DB 541 ACI 543

RESULT 3
AAB08849
ID AAB08849 standard; protein; 543 AA.
XX
AC AAB08849;
XX
DT 15-JAN-2001 (first entry)
XX
DE Amino acid sequence of a human heparanase polypeptide.
XX
KW Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
KW heparin-binding growth factor; cytokine; neurodegenerative plaque;
KW wound healing; infection; burn; angiogenesis; restenosis;
KW atherosclerosis; inflammation; neurodegenerative disease;
KW Gerstmann-Strausler Syndrome; Creutzfeldt-Jakob disease.
XX
OS Homo sapiens.
XX
PN MO20052178-A1.
XX
PD 08-SEP-2000.
XX
PF 14-FEB-2000; 2000MO-US003542.
XX
PR 01-MAR-1999; 99US-00258892.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASTI MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.
XX
PI Pecker I, Vlodevsky I, Feinstein E;
XX
XX WPI; 2000-579289/54.
DR N-PSDB; AAA75051.
XX
PT New polynucleotides encoding a polypeptide having heparanase activity,
PT useful in wound healing and in gene therapy, particularly in treating
PT tumor, inflammation, autoimmunity, neurodegenerative diseases.
XX
XX Claim 22; Fig 1; 152pp; English.
XX
PS The present sequence represents a human protein with heparanase catalytic
CC activity. The heparanase (hpa) polynucleotide is useful in gene therapy,
CC particularly in treating tumour, inflammation or autoimmunity.
CC Particularly, the polynucleotide is useful in modulating the
CC bioavailability of heparin-binding growth factors, cellular responses to
CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
CC interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular
CC susceptibility to certain viral and some bacterial and protozoa
CC infections, or disintegration of neurodegenerative plaques. The
CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or
CC radiation burns), and in the treatment of angiogenesis, restenosis,
CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
CC Strausler Syndrome or Creutzfeldt-Jakob disease), and some viral,
CC bacterial or protozoa infections

XX SQ Sequence 543 AA;
Query Match 100.0%; Score 2842; DB 3; Length 543;
Best Local Similarity 100.0%; Pred. No. 2, 5e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLTSSKRALPPPLMLLLGLGPIPSGALPPPAQADVDVDFPQEPHLVSPFLSVT 60
DB 1 MLTSSKRALPPPLMLLLGLGPIPSGALPPPAQADVDVDFPQEPHLVSPFLSVT 60
QY 61 IDANLATDPRRLILGSPKLTTLARGLSPAYLREGTKTDFLIPDKKESFEEBSYQOS 120
DB 61 IDANLATDPRRLILGSPKLTTLARGLSPAYLREGTKTDFLIPDKKESFEEBSYQOS 120
QY 121 QVNODICKYGSIPPDVEBKRLLEWRYQOQLLRHHYOKKPKNSTYSSSVUVLYTFANCS 180
DB 121 QVNODICKYGSIPPDVEBKRLLEWRYQOQLLRHHYOKKPKNSTYSSSVUVLYTFANCS 180
QY 181 GLDLIFGLNMLRTADIQMNSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
DB 181 GLDLIFGLNMLRTADIQMNSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
QY 241 QLGEDYIQLHKLTKSKSTFKNAKLYGPDVGQPRRKTAKMLSLKAGGEVIDSVTMHHYLL 300
DB 241 QLGEDYIQLHKLTKSKSTFKNAKLYGPDVGQPRRKTAKMLSLKAGGEVIDSVTMHHYLL 300
QY 301 NGRTATBEDPLNDVLDIFISSVOKVQVVESTPPGKKWLGERTSSAYGGAPLLSTFA 360
DB 301 NGRTATBEDPLNDVLDIFISSVOKVQVVESTPPGKKWLGERTSSAYGGAPLLSTFA 360
QY 361 AGFWMLDLGLGSARWGIEVWNRQVFGAGNYHLVDENFDPLPDYWLSTLFFKKLVGTXYLM 420
DB 361 AGFWMLDLGLGSARWGIEVWNRQVFGAGNYHLVDENFDPLPDYWLSTLFFKKLVGTXYLM 420
QY 421 ASVQGSKRKRKLRYVYLHCTNTDNPARYKEGDLTLVAIINLHNVTKYLRLPYFPSNKOVDXYLL 480
DB 421 ASVQGSKRKRKLRYVYLHCTNTDNPARYKEGDLTLVAIINLHNVTKYLRLPYFPSNKOVDXYLL 480
QY 481 RPLGPHGLLSKSVQVNLGLTLKAVDDQTLPLMEKPLRGGSLGLPAFYSFFVIRNAKVA 540
DB 481 RPLGPHGLLSKSVQVNLGLTLKAVDDQTLPLMEKPLRGGSLGLPAFYSFFVIRNAKVA 540
QY 541 ACI 543
DB 541 ACI 543

RESULT 4
AA52990
ID AA52990 standard; protein; 543 AA.
XX
AC AA52990;
XX
DT 21-FEB-2000 (first entry)
XX
DE Human heparanase protein sequence.
XX
KW Human; heparanase; hpa; diagnosis; therapy; tumour; cytostatic;
KW antidiabetic; immunomodulatory; anti-inflammatory; nephrotic;
KW metastasis; adenocarcinoma; squamous cell carcinoma; teratocarcinoma;
KW mesothelioma; melanoma; lymphoma; leukemia; cancer; sepsis; diabetes;
KW inflammation; haemorrhagic nephritis; nephrotic syndrome;
KW autoimmune disease; anticancer; kidney disease.
XX
OS Homo sapiens.
XX
PN MO3957153-A1.
XX
PD 11-NOV-1999.
XX
PF 29-APR-1999; 99WO-US009255.
XX

PR 01-MAY-1998; 98US-00071739.

XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASI MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.

XX Pecker I, Vlodavsky I, Friedman Y, Perets T;

XX WPI; 2000-052944/04.

DR N-PSDB; AA233290.

XX Heparanase-specific molecular probes useful for diagnosis and treatment,
XX e.g. of tumors, and for targeted drug delivery.

XX Example; Page 81-82; 90pp; English.

XX The present invention describes heparanase-specific molecular probes,
XX useful for methods of detecting heparanase in situ. The probes and anti-
XX heparanase antibodies are used to detect or quantify the expression of
XX heparanase, for diagnosis and monitoring of diseases (especially
XX metastasis), for treatment of heparanase-associated diseases (e.g.
XX tumors, (adeno)carcinoma, squamous cell carcinoma, teratocarcinoma,
XX mesothelioma, melanoma, lymphoma or leukemia, a solid cancer (or its
XX metastases) derived from liver, prostate, bladder, breast, ovary, cervix,
XX colon, skin, intestine, stomach, uterus and pancreas, kidney disease,
XX diabetes and inflammation, haemorrhagic nephritis, nephrotic syndrome,
XX sepsis and inflammatory or autoimmune disease), for targeted drug
XX delivery (e.g. of anticancer agents) and as research reagents. The
XX present sequence represents human heparanase, which is used in the
XX exemplification of the present invention

XX Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 3; Length 543;

Best Local Similarity 100.0%; Pred. No. 2.5e-273; Mismatches 0; Indels 0; Gaps 0;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLIRSKPALPPMLILGIPGLSPGALPRPAQADVVDDPFTQEPHLIVSPFLSVT 60

DB 1 MLIRSKPALPPMLILGIPGLSPGALPRPAQADVVDDPFTQEPHLIVSPFLSVT 60

QY 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFSGITDPLIDPKKESTFEERSYWG 120

DB 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFSGITDPLIDPKKESTFEERSYWG 120

QY 121 QVNODICKYGSIPDVEEKLRLWPYQOLLRHYQKKFNSTYSRSVDVLYTFANCS 180

DB 121 QVNODICKYGSIPDVEEKLRLWPYQOLLRHYQKKFNSTYSRSVDVLYTFANCS 180

QY 181 GLDLIFGLNALIRTDLQWNSNAQLLDYCSSKGYNI SWEIGNEPNSFLKKADIFINGS 240

DB 181 GLDLIFGLNALIRTDLQWNSNAQLLDYCSSKGYNI SWEIGNEPNSFLKKADIFINGS 240

QY 241 QLGEDYIQLHLKLRSTFKNAKLYGPDVGOPRRKTATMLKSPFKAGEVIVDSVTHHYYL 300

DB 241 QLGEDYIQLHLKLRSTFKNAKLYGPDVGOPRRKTATMLKSPFKAGEVIVDSVTHHYYL 300

QY 301 NGRTATREDPLNPVDLIFISSVQKVFQVVESTPGKKWLGETSSAYGGAPLSDTFA 360

DB 301 NGRTATREDPLNPVDLIFISSVQKVFQVVESTPGKKWLGETSSAYGGAPLSDTFA 360

QY 361 AGFWMLDKLGLSARMGIEVMRQVFGAGNYHLVDENFPLPYWISLFLKKLVGTKVL 420

DB 361 AGFWMLDKLGLSARMGIEVMRQVFGAGNYHLVDENFPLPYWISLFLKKLVGTKVL 420

QY 421 ASVQGSRRRLRYVLIHCTNTDNPYKEGDLTYAINLHNTKYLRPLYPFSNFQVQKYL 480

DB 421 ASVQGSRRRLRYVLIHCTNTDNPYKEGDLTYAINLHNTKYLRPLYPFSNFQVQKYL 480

QY 481 RPLGPHGLLSKSVQNLTLKAVDDOTLPLMEKPLRPSSGLPAFVSFFVIRNAKYA 540

DB 481 RPLGPHGLLSKSVQNLTLKAVDDOTLPLMEKPLRPSSGLPAFVSFFVIRNAKYA 540

QY 541 ACI 543
DB 541 ACI 543

RESULT 5
ID AAY97635
AAY97635 standard; protein; 543 AA.

XX AAY97635;

XX 20-APR-2001 (first entry)

XX Human heparanase protein sequence.

XX Heparanase; hnp1; wound healing; angiogenesis; restenosis; Scarpe;
XX atherosclerosis; inflammation; pulmonary disease; Alzheimer's disease;
XX neurodegenerative disease; Creutzfeldt-Jakob disease; viral infection;
XX gene therapy; human.

XX Homo sapiens.

XX W020010643-A2.

XX 04-JAN-2001.

XX 19-JUN-2000; 2000WO-11000358.

XX 25-JUN-1999; 99US-0140801P.

XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.

XX Pecker I, Michal I, Itzhaki H;

XX WPI; 2001-137930/14.

XX New polynucleotides and polypeptides that are distantly homologous to
XX heparanase, useful in wound healing, as well as in gene therapy protocols
XX for angiogenesis, restenosis, atherosclerosis, or inflammation.

XX Disclosure; Page 64-65; 67pp; English.

XX This sequence represents a heparanase of the invention. The heparanase
XX DNA and protein sequences are useful in wound healing, angiogenesis,
XX restenosis, atherosclerosis, inflammation, pulmonary diseases,
XX neurodegenerative diseases (such as Scarpe, Alzheimer's disease, and
XX Creutzfeldt-Jakob disease) or viral infections. The heparanase coding
XX sequence is particularly useful in gene therapy

XX Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 4; Length 543;

Best Local Similarity 100.0%; Pred. No. 2.5e-273; Mismatches 0; Indels 0; Gaps 0;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLIRSKPALPPMLILGIPGLSPGALPRPAQADVVDDPFTQEPHLIVSPFLSVT 60

DB 1 MLIRSKPALPPMLILGIPGLSPGALPRPAQADVVDDPFTQEPHLIVSPFLSVT 60

QY 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFSGITDPLIDPKKESTFEERSYWG 120

DB 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFSGITDPLIDPKKESTFEERSYWG 120

QY 121 QVNODICKYGSIPDVEEKLRLWPYQOLLRHYQKKFNSTYSRSVDVLYTFANCS 180

DB 121 QVNODICKYGSIPDVEEKLRLWPYQOLLRHYQKKFNSTYSRSVDVLYTFANCS 180

QY 181 GLDLIFGLNALIRTDLQWNSNAQLLDYCSSKGYNI SWEIGNEPNSFLKKADIFINGS 240

DB 181 GLDLIFGLNALIRTDLQWNSNAQLLDYCSSKGYNI SWEIGNEPNSFLKKADIFINGS 240

QY 241 QLGEDYIQLHLKLRSTFKNAKLYGPDVGOPRRKTATMLKSPFKAGEVIVDSVTHHYYL 300

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Db      241 QLGEDYIQLHKLKSTFKNAKLYGPDVGQRRRTAKMLKSLKAGEVIDSVTMHHYYL 300
Qy      301 NGRTATREDPLNPVDLFISSVQKVFQVVESTPRGKKVWLGENTSAYGGAPLLSDTFA 360
Db      301 NGRTATREDPLNPVDLFISSVQKVFQVVESTPRGKKVWLGENTSAYGGAPLLSDTFA 360
Qy      361 AGFWMLDKLGISARMGIEVVNRQVFFGAGNHLVDENEDPLPDYWSLLPFKKLVGTXYLM 420
Db      361 AGFWMLDKLGISARMGIEVVNRQVFFGAGNHLVDENEDPLPDYWSLLPFKKLVGTXYLM 420
Qy      421 ASVQSSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYRLPYPSNKOVDKXYL 480
Db      421 ASVQSSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYRLPYPSNKOVDKXYL 480
Qy      481 RPLGPHGLSKSVQNLGLTLKMWDDQTLPLMEKPLRPGSSLG.PAFSYSFFVIRNAKVA 540
Db      481 RPLGPHGLSKSVQNLGLTLKMWDDQTLPLMEKPLRPGSSLG.PAFSYSFFVIRNAKVA 540
Qy      541 ACI 543
Db      541 ACI 543

RESULT 6
ABB07813
ID      ABB07813 standard; protein; 543 AA.
XX      ABB07813;
DT      03-JUL-2002 (first entry)
XX      Human heparanase sequence.
DE      Heparanase; catalytic; cytosolic; antiviral; antibacterial; enzyme;
KM      anti-Protozoan; neuroprotective; heparin; human.
XX      Homo sapiens.
XX      Key      Location/Qualifiers
FT      Peptide      1..35
FT      Protein      /note= "signal peptide"
FT      Protein      36..543
FT      Protein      /note= "mature protein"
XX      US2002034810-A1.
XX      21-MAR-2002.
XX      16-AUG-2001; 2001US-00930218.
XX      20-SEP-2000; 2000US-00666390.
XX      (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX      Goldsmith O, Pecker I, Vlodavsky I, Michal I, Zcharia E;
XX      WPI; 2002-338926/37.
XX      Nucleic acid encoding avian and reptile heparanase polypeptide is useful
XX      to treat various heparin-related disorders and the signal peptide is
XX      useful in production of membrane-targeted or secreted recombinant
XX      proteins.
XX      Disclosure; Fig 1a; 39pp; English.
XX      The invention relates to an isolated avian and reptile nucleic acid,
XX      encoding a polypeptide with heparanase catalytic activity. The signal
XX      peptide of the nucleic acid can be used to express membrane-associated or
XX      secreted proteins in heterologous expression systems. The encoded
XX      polypeptides can be used to prevent tumour angiogenesis, metastasis and
XX      invasion, and to intervene with pathologies associated with impaired
XX      heparin-binding growth factors, cellular responses to heparin-binding
XX      growth factors and cytokines, cell interaction with plasma lipoproteins,

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CC      cellular susceptibility to viral, protozoa and bacterial infections or
CC      disintegration of neurodegenerative plaques. The present sequence
CC      represents a human heparanase protein sequence used in similarity studies
XX      Sequence 543 AA;
XX      Query Match      100.0%; Score 2842; DB 5; Length 543;
XX      Best Local Similarity 100.0%; Pred. No. 2,5e-473;
XX      Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 MLRSKDALPPMLLLGLPLGRLSPALPPPAQAOVVDLDFPTQEPRLHVSQSFISVT 60
Db      1 MLRSKDALPPMLLLGLPLGRLSPALPPPAQAOVVDLDFPTQEPRLHVSQSFISVT 60
Qy      61 IDANLATDPPELILGSPKRLTLAGISPAVLRGSGTKTDLIDPKKESEFEERSYQOS 120
Db      61 IDANLATDPPELILGSPKRLTLAGISPAVLRGSGTKTDLIDPKKESEFEERSYQOS 120
Qy      121 QVNODICKYGSIPPDVEKRLLEWPYOEOLLRHHYOKKFKNSTYSRSVDVLYTFANCS 180
Db      121 QVNODICKYGSIPPDVEKRLLEWPYOEOLLRHHYOKKFKNSTYSRSVDVLYTFANCS 180
Qy      181 GLDLIFGLNALRLTADLQMNSSNAQLLDYCSKGYNI SWELGNEPNSFLKKADIFINGS 240
Db      181 GLDLIFGLNALRLTADLQMNSSNAQLLDYCSKGYNI SWELGNEPNSFLKKADIFINGS 240
Qy      241 QLGEDYIQLHKLKSTFKNAKLYGPDVGQRRRTAKMLKSLKAGEVIDSVTMHHYYL 300
Db      241 QLGEDYIQLHKLKSTFKNAKLYGPDVGQRRRTAKMLKSLKAGEVIDSVTMHHYYL 300
Qy      301 NGRTATREDPLNPVDLFISSVQKVFQVVESTPRGKKVWLGENTSAYGGAPLLSDTFA 360
Db      301 NGRTATREDPLNPVDLFISSVQKVFQVVESTPRGKKVWLGENTSAYGGAPLLSDTFA 360
Qy      361 AGFWMLDKLGISARMGIEVVNRQVFFGAGNHLVDENEDPLPDYWSLLPFKKLVGTXYLM 420
Db      361 AGFWMLDKLGISARMGIEVVNRQVFFGAGNHLVDENEDPLPDYWSLLPFKKLVGTXYLM 420
Qy      421 ASVQSSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYRLPYPSNKOVDKXYL 480
Db      421 ASVQSSKRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNVTKYRLPYPSNKOVDKXYL 480
Qy      481 RPLGPHGLSKSVQNLGLTLKMWDDQTLPLMEKPLRPGSSLG.PAFSYSFFVIRNAKVA 540
Db      481 RPLGPHGLSKSVQNLGLTLKMWDDQTLPLMEKPLRPGSSLG.PAFSYSFFVIRNAKVA 540
Qy      541 ACI 543
Db      541 ACI 543

RESULT 7
ADG88800
ID      ADG88800 standard; protein; 543 AA.
XX      ADG88800;
XX      11-MAR-2004 (first entry)
XX      Human hpa protein.
XX      Wound healing; heparanase; ulcer; burn; laceration; surgical incision;
XX      necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy.
XX      Homo sapiens.
XX      US2003161823-A1.
XX      28-AUG-2003.
XX      14-JAN-2003; 2003US-00341582.
XX      31-AUG-1998; 98WO-US017954.

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PR 01-MAR-1999; 99US-00258892.
 PR 06-FEB-2001; 2001US-00776874.
 PR 05-SEP-2001; 2001US-00776874.
 PR 19-NOV-2001; 2001US-00988113.

PA (ILAN/) ILAN N.
 PA (VLAD/) VLADAVSKY I.
 PA (YACO/) YACOBZ-ZEEVI O.
 PA (PECK/) PECKER I.
 PA (FEIN/) FEINSTEIN E.

PI Ian N, Vladavsky I, Yacoby-Zeevi O, Pecker I, Feinstein E;

DR MPI: 2003-897910/82.

DR N-FSDB: ADG88799, ADG88801, ADG88832.

PT Composition for treating a wound comprising recombinant heparanase is
 PT useful to induce or accelerate wound healing and induce or accelerate
 XX angiogenesis.

PS Claim 2; SEQ ID NO 10; 143bp; English.

CC The present invention relates to methods and compositions for inducing
 CC and/or accelerating wound healing via the catalytic activity of
 CC heparanase. The invention is used to induce or accelerate a healing
 CC process, particularly of an ulcer, burn, laceration, surgical incision,
 CC necrosis, pressure wound, diabetic ulcer and to induce or accelerate
 CC angiogenesis. The present sequence is human hpa protein.

XX Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 7; Length 543;
 Best Local Similarity 100.0%; Pred. No. 2,5e-273;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSXPALPPPLMLLLGLPLGSPALPPAQAQDVVDLDFFOBPPLHVSBSFISVT 60
 DB 1 MLRSXPALPPPLMLLLGLPLGSPALPPAQAQDVVDLDFFOBPPLHVSBSFISVT 60
 QY 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFGGTITDPLIDPKKESFEEBSYWQS 120
 DB 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFGGTITDPLIDPKKESFEEBSYWQS 120
 QY 121 QVNODICKGSIIPDVEEKLRLWEPYOEQLLREHYOKKFNSTYSR8SVUYTPANC8 180
 DB 121 QVNODICKGSIIPDVEEKLRLWEPYOEQLLREHYOKKFNSTYSR8SVUYTPANC8 180
 QY 181 GDDLIFGLNALILRTADLQWNSNMAQLLDYCSKGYNISWELGNEPNSFLKADIFINGS 240
 DB 181 GDDLIFGLNALILRTADLQWNSNMAQLLDYCSKGYNISWELGNEPNSFLKADIFINGS 240
 QY 241 QLEGDYIOLHLKLRKSTFKNAKLYGPDVGQPRRTAKMLKSFKAAGEVIDSTWHNYL 300
 DB 241 QLEGDYIOLHLKLRKSTFKNAKLYGPDVGQPRRTAKMLKSFKAAGEVIDSTWHNYL 300
 QY 301 NGRTATREDPFLNPVDLDFISSVOKYQVVESTPRGKWLGETSSAYGGAPLSDTRA 360
 DB 301 NGRTATREDPFLNPVDLDFISSVOKYQVVESTPRGKWLGETSSAYGGAPLSDTRA 360
 QY 361 AGFWMLDRLGLSABMGIEVWVRQYFPGAGNYHLYDENFDELPRYWSLFLPKLVGTVM 420
 DB 361 AGFWMLDRLGLSABMGIEVWVRQYFPGAGNYHLYDENFDELPRYWSLFLPKLVGTVM 420
 QY 421 ASVGGSRKRLRYVLAHCTNTDNPRYKGGDLTYAIVMLHNTKYLRLPYPSNKQVDKYL 480
 DB 421 ASVGGSRKRLRYVLAHCTNTDNPRYKGGDLTYAIVMLHNTKYLRLPYPSNKQVDKYL 480
 QY 481 RPLGPHGLSKSVQVNLGLTKQVDDOTLPLMKELRPSSSLGPAFYSYFVFINAKYA 540
 DB 481 RPLGPHGLSKSVQVNLGLTKQVDDOTLPLMKELRPSSSLGPAFYSYFVFINAKYA 540
 QY 541 ACT 543
 DB 541 ACT 543

DB 541 ACT 543

RESULT 8

ID ADL16379 standard; protein; 543 AA.

AC ADL16379;

DT 06-MAY-2004 (first entry)

DE Human heparanase partial protein.

KW Human; heparanase; heparanase-dependent cancer; cancer;
 KW autoimmune reaction; inflammation; chromosome 4; enzyme.

OS Homo sapiens.

PN US2003236215-A1.

PD 25-DEC-2003.

PF 09-JUN-2003; 2003US-00456573.

PR 31-AUG-1998; 98MO-US017954.

PR 01-MAR-1999; 99US-00258892.

PR 08-NOV-1999; 99US-00435739.

PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
 (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

PI Pecker I, Vladavsky I, Feinstein E;

DR MPI: 2004-070610/07.

PT New antisense oligonucleotide hybridizable with a polynucleotide encoding
 PT a polypeptide with heparanase activity, useful for treating diseases such
 PT as cancer and autoimmune disorders.

PS Claim 3; SEQ ID NO 10; 108bp; English.

CC The invention relates to an antisense oligonucleotide (ASO) comprising a
 CC polynucleotide or a polynucleotide analogue of at least 10 bases being
 CC hybridizable in vivo, under physiological conditions, with a portion of
 CC a polynucleotide strand encoding a polypeptide having heparanase
 CC catalytic activity. Also included are a method of in vivo downregulating
 CC heparanase activity (comprising administering the ASO in vivo), a method
 CC (characterized by heparanase activity, comprising administering ASO to
 CC the subject), a pharmaceutical composition comprising the ASO and a
 CC carrier, an antisense nucleic acid construct (comprising a promoter
 CC antisense RNA sequence of at least 10 bases being hybridizable in vivo,
 CC under physiological conditions, with a polynucleotide strand encoding a
 CC polypeptide having heparanase catalytic activity), a method of in vivo
 CC downregulating heparanase activity (comprising administering in vivo the
 CC antisense nucleic acid construct), a pharmaceutical composition
 CC comprising the antisense nucleic acid construct and a carrier, and an
 CC analogue of at least 10 bases being hybridizable in vivo, under
 CC physiological conditions, with a portion of a polynucleotide strand being
 CC characterized by forming at least a portion of an untranslated region
 CC (UTR) for a polynucleotide strand encoding a polypeptide having
 CC heparanase catalytic activity. The methods and compositions of the
 CC present invention are useful for the prevention and/or treatment of
 CC diseases or conditions associated with aberrant heparanase activity, such
 CC as heparanase-dependent cancer, cancer, autoimmune reaction and
 CC inflammation. The gene for human heparanase is located on chromosome 4.
 CC The present sequence is a human heparanase protein.

XX Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 8; Length 543;

Best Local Similarity 100.0%; Pred. No. 2.5e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MLRSKRALPPRLMLLLGLPLSPGALPRPAQADVDLDFPTQEPHLHVSFSLSVT 60
DB      1 MLRSKRALPPRLMLLLGLPLSPGALPRPAQADVDLDFPTQEPHLHVSFSLSVT 60
QY      61 IDANLATDPRFLILGSPKLTARGLSPAYLRFSGTGTDFLIPDKKESFTEERSYQOS 120
DB      61 IDANLATDPRFLILGSPKLTARGLSPAYLRFSGTGTDFLIPDKKESFTEERSYQOS 120
QY      121 QVNODICKYGSIPPDVEEKLRLWPYQOQLLREHYOKKFNSTYSRSADVLYTFANCS 180
DB      121 QVNODICKYGSIPPDVEEKLRLWPYQOQLLREHYOKKFNSTYSRSADVLYTFANCS 180
QY      181 GLDLIFGIALLRTPADLQWSSNAQLLDYCSSKGYNI SWELGNBPNSFLKKAIDIFINGS 240
DB      181 GLDLIFGIALLRTPADLQWSSNAQLLDYCSSKGYNI SWELGNBPNSFLKKAIDIFINGS 240
QY      241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRKRTAKMLKSFLLKAGGEVIDSVTHHHYLL 300
DB      241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRKRTAKMLKSFLLKAGGEVIDSVTHHHYLL 300
QY      301 NGRTATREDPLNPVDLDFISSVQKVFQVESTTRPGKVMLGETSAYGGAPLLSDTFA 360
DB      301 NGRTATREDPLNPVDLDFISSVQKVFQVESTTRPGKVMLGETSAYGGAPLLSDTFA 360
QY      361 AGFPMWLDLGLSARNGIEVMRQVFGAGNHYLVDENDPLPDYVLSLFPKLVGTXYLM 420
DB      361 AGFPMWLDLGLSARNGIEVMRQVFGAGNHYLVDENDPLPDYVLSLFPKLVGTXYLM 420
QY      421 ASVQSKRRKRLRVYLHCTNTDNPFRYKEGDLTYAINLHNTKYLRPYPFNSKQVDKXLL 480
DB      421 ASVQSKRRKRLRVYLHCTNTDNPFRYKEGDLTYAINLHNTKYLRPYPFNSKQVDKXLL 480
QY      481 RPLGPHGLSKSVQNLGLTLKXVDDQTLPLMEKPLRPGSSLGIPAFSYSPFVIRNAKVA 540
DB      481 RPLGPHGLSKSVQNLGLTLKXVDDQTLPLMEKPLRPGSSLGIPAFSYSPFVIRNAKVA 540
QY      541 ACI 543
DB      541 ACI 543

RESULT 9
ADM48716
ID ADM48716 standard; protein; 543 AA.
AC ADM48716;
XX      03-JUN-2004 (first entry)
DE      Human hpa protein #1.
XX      Transgenic animal; heparanase; cancer; viral infection; restenosis;
KW      neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;
KW      human.
XX      Homo sapiens.
OS      US2003217375-A1.
PN      20-NOV-2003.
PD      24-FEB-2003; 2003US-00371218.
PE      31-AUG-1998; 98MO-US017954.
PR      01-MAR-1999; 98US-00258892.
PR      06-FEB-2001; 2001US-0076874.
PR      19-NOV-2001; 2001US-00986113.
XX      (ZCHARA/) ZCHARA E.
PA      (VL0D/) VL0DAVSKY I.

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PA      (METZ/) METZGER S.
PA      (PECK/) PECKER I.
PA      (ILAN/) ILAN N.
PA      (CHAJEK-SHAUL T.
PA      (GOLD/) GOLDSHMIDT O.
PI      Zcharia E, Vlodayevsky I, Metzger S, Pecker I, Ilan N;
PI      Chajek-Shaul T, Goldshmidt O;
DR      WPI; 2004-021918/02.
DR      N-PSDB; ADM48715, ADM48717.
XX      New transgenic non-human animal expressing heparinase, useful as models
XX      for human disease, such as cancers, viral infection, neurodegenerative
XX      diseases, restenosis, atherosclerosis and pulmonary disorders.
XX      Example 1; SEQ ID NO 10; 106pp; English.
XX      The present invention relates to a transgenic non-human animal whose
XX      genome comprises an exogenous polynucleotide sequence, including a
XX      promoter active in tissues of the non-human, a region encoding a human
XX      heparanase, where the promoter and the region encoding human heparanase
XX      are operably linked in the exogenous polynucleotide such that human
XX      heparanase is expressed in at least a portion of the cells of the non-
XX      human animal. The methods and compositions of the present invention are
XX      useful for the production of transgenic animals expressing heparanase, to
XX      be used as models for human diseases such as cancers, viral infection,
XX      restenosis, neurodegenerative diseases, atherosclerosis and pulmonary
XX      disorders. The present sequence is human hpa protein used in the
XX      exemplification of the invention.

```

Seq Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 8; Length 543;
Best Local Similarity 100.0%; Pred. No. 2.5e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 MLRSKRALPPRLMLLLGLPLSPGALPRPAQADVDLDFPTQEPHLHVSFSLSVT 60
DB      1 MLRSKRALPPRLMLLLGLPLSPGALPRPAQADVDLDFPTQEPHLHVSFSLSVT 60
QY      61 IDANLATDPRFLILGSPKLTARGLSPAYLRFSGTGTDFLIPDKKESFTEERSYQOS 120
DB      61 IDANLATDPRFLILGSPKLTARGLSPAYLRFSGTGTDFLIPDKKESFTEERSYQOS 120
QY      121 QVNODICKYGSIPPDVEEKLRLWPYQOQLLREHYOKKFNSTYSRSADVLYTFANCS 180
DB      121 QVNODICKYGSIPPDVEEKLRLWPYQOQLLREHYOKKFNSTYSRSADVLYTFANCS 180
QY      181 GLDLIFGIALLRTPADLQWSSNAQLLDYCSSKGYNI SWELGNBPNSFLKKAIDIFINGS 240
DB      181 GLDLIFGIALLRTPADLQWSSNAQLLDYCSSKGYNI SWELGNBPNSFLKKAIDIFINGS 240
QY      241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRKRTAKMLKSFLLKAGGEVIDSVTHHHYLL 300
DB      241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRKRTAKMLKSFLLKAGGEVIDSVTHHHYLL 300
QY      301 NGRTATREDPLNPVDLDFISSVQKVFQVESTTRPGKVMLGETSAYGGAPLLSDTFA 360
DB      301 NGRTATREDPLNPVDLDFISSVQKVFQVESTTRPGKVMLGETSAYGGAPLLSDTFA 360
QY      361 AGFPMWLDLGLSARNGIEVMRQVFGAGNHYLVDENDPLPDYVLSLFPKLVGTXYLM 420
DB      361 AGFPMWLDLGLSARNGIEVMRQVFGAGNHYLVDENDPLPDYVLSLFPKLVGTXYLM 420
QY      421 ASVQSKRRKRLRVYLHCTNTDNPFRYKEGDLTYAINLHNTKYLRPYPFNSKQVDKXLL 480
DB      421 ASVQSKRRKRLRVYLHCTNTDNPFRYKEGDLTYAINLHNTKYLRPYPFNSKQVDKXLL 480
QY      481 RPLGPHGLSKSVQNLGLTLKXVDDQTLPLMEKPLRPGSSLGIPAFSYSPFVIRNAKVA 540
DB      481 RPLGPHGLSKSVQNLGLTLKXVDDQTLPLMEKPLRPGSSLGIPAFSYSPFVIRNAKVA 540

```


XX Claim 22; Page 122-123; 152pp; English.

CC The present sequence represents a human protein with heparanase catalytic
XX activity. The heparanase (hpa) polynucleotide is useful in gene therapy,
CC particularly in treating tumour, inflammation or autoimmunity.
CC Particularly, the polynucleotide is useful in modulating the
CC bioavailability of heparin-binding growth factors, cellular responses to
CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
CC interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular
CC susceptibility to certain viral and some bacterial and protozoa
CC infections, or disintegration of neurodegenerative plaques. The
CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or
CC radiation burns), and in the treatment of angiogenesis, restenosis,
CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
CC Strausler Syndrome or Creutzfeldt-Jakob disease), and some viral,
CC bacterial or protozoa infections

XX Sequence 592 AA;

Query Match 100.0%; Score 2842; DB 3; Length 592;

Best Local Similarity 100.0%; Pred. No. 2.9e-273; Indels 0; Gaps 0;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKRALPPMLLLGLPLSPGALPPPAQADVDDFTQEPHLHVSFSLSVT 60
DB 50 MLRSKRALPPMLLLGLPLSPGALPPPAQADVDDFTQEPHLHVSFSLSVT 109
QY 61 IDANLATDPRLLILGSPKLTARGLSPAYLRFSGTDTDLIFDPKKESTFEERSYQOS 120
DB 110 IDANLATDPRLLILGSPKLTARGLSPAYLRFSGTDTDLIFDPKKESTFEERSYQOS 169
QY 121 QVNODICKYGSIPPDVEEKLRLFWPYQOLLRHYQKKFNKSTYSRSVDVLYTFANCS 180
DB 170 QVNODICKYGSIPPDVEEKLRLFWPYQOLLRHYQKKFNKSTYSRSVDVLYTFANCS 229
QY 181 GLDLIFGLNALRLTADLQWSSNAQLLDYCSSKGYNSWELGNEPNSFLKKADIFINGS 240
DB 230 GLDLIFGLNALRLTADLQWSSNAQLLDYCSSKGYNSWELGNEPNSFLKKADIFINGS 289
QY 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 300
DB 290 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 349
QY 301 NGRTATREDPLNPVLDLIFISSVQKVPQVVESTRGKKVWLGFTSSAYGGGAPLLSDTFA 360
DB 350 NGRTATREDPLNPVLDLIFISSVQKVPQVVESTRGKKVWLGFTSSAYGGGAPLLSDTFA 409
QY 361 AGFMWLDKLGASARWGEIWMKQVFFGAGNYLVDENFDPLPDYWSLLFKLVGTXYLM 420
DB 410 AGFMWLDKLGASARWGEIWMKQVFFGAGNYLVDENFDPLPDYWSLLFKLVGTXYLM 469
QY 421 ASVQSSKRRKRLVYLHCTNTDNPAYKEGDLTYAINTLHNTCYLRLPYFNSKQVDTXYL 480
DB 470 ASVQSSKRRKRLVYLHCTNTDNPAYKEGDLTYAINTLHNTCYLRLPYFNSKQVDTXYL 529
QY 481 RPLGSHGLLSKSVQVNGTLKXVNDQDTPLPMEKELRPGSSGLPAFSYSPVFINNAYYA 540
DB 530 RPLGSHGLLSKSVQVNGTLKXVNDQDTPLPMEKELRPGSSGLPAFSYSPVFINNAYYA 589
QY 541 ACI 543
DB 590 ACI 592

RESULT 12
ADG88804
ID ADG88804 standard; protein; 592 AA.

XX ADG88804;
XX
XX 11-MAR-2004 (first entry)
XX

DE Human SK-hep1 protein.

XX Wound healing; heparanase; ulcer; burn; laceration; surgical incision;
KW necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy.

XX Homo sapiens.

XX US2003161823-A1.

XX 28-AUG-2003.

XX 14-JAN-2003; 2003US-00341582.

XX 31-AUG-1998; 98WO-US017954.

XX 01-MAR-1999; 99US-00258892.

XX 06-FEB-2001; 2001US-00776874.

XX 05-SEP-2001; 2001WO-IL000830.

XX 19-NOV-2001; 2001US-00988113.

XX (ILAN/) ILAN N.

XX (VLOD/) VLODAVSKY I.

XX (YACO/) YACOBY-ZEEVI O.

XX (PECK/) PECKER I.

XX (FEIN/) FEINSTEIN E.

XX Ilan N, Vlodavsky I, Yacoby-Zeevi O, Pecker I, Feinstein E;

XX WPI; 2003-897910/82.

XX N-PSDB; ADG88803, ADG88805.

XX Composition for treating a wound comprising recombinant heparanase is

XX useful to induce or accelerate wound healing and induce or accelerate

XX angiogenesis.

XX Claim 2; SEQ ID NO 14; 143pp; English.

XX The present invention relates to methods and compositions for inducing

XX and/or accelerating wound healing via the catalytic activity of

XX heparanase. The invention is used to induce or accelerate a healing

XX process, particularly of an ulcer, burn, laceration, surgical incision,

XX necrosis, pressure wound, diabetic ulcer and to induce or accelerate

XX angiogenesis. The present sequence is human SK-hep1 protein.

XX Sequence 592 AA;

Query Match 100.0%; Score 2842; DB 7; Length 592;

Best Local Similarity 100.0%; Pred. No. 2.9e-273; Indels 0; Gaps 0;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKRALPPMLLLGLPLSPGALPPPAQADVDDFTQEPHLHVSFSLSVT 60
DB 50 MLRSKRALPPMLLLGLPLSPGALPPPAQADVDDFTQEPHLHVSFSLSVT 109
QY 61 IDANLATDPRLLILGSPKLTARGLSPAYLRFSGTDTDLIFDPKKESTFEERSYQOS 120
DB 110 IDANLATDPRLLILGSPKLTARGLSPAYLRFSGTDTDLIFDPKKESTFEERSYQOS 169
QY 121 QVNODICKYGSIPPDVEEKLRLFWPYQOLLRHYQKKFNKSTYSRSVDVLYTFANCS 180
DB 170 QVNODICKYGSIPPDVEEKLRLFWPYQOLLRHYQKKFNKSTYSRSVDVLYTFANCS 229
QY 181 GLDLIFGLNALRLTADLQWSSNAQLLDYCSSKGYNSWELGNEPNSFLKKADIFINGS 240
DB 230 GLDLIFGLNALRLTADLQWSSNAQLLDYCSSKGYNSWELGNEPNSFLKKADIFINGS 289
QY 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 300
DB 290 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 349
QY 301 NGRTATREDPLNPVLDLIFISSVQKVPQVVESTRGKKVWLGFTSSAYGGGAPLLSDTFA 360
DB 350 NGRTATREDPLNPVLDLIFISSVQKVPQVVESTRGKKVWLGFTSSAYGGGAPLLSDTFA 409

QY 361 AGFMWLDKLGASARMGIEVVRQVFFGAGNHYLVNDENPDLDPDWLSLFFPKLVGTXYLM 420
DB 410 AGFMWLDKLGASARMGIEVVRQVFFGAGNHYLVNDENPDLDPDWLSLFFPKLVGTXYLM 469
QY 421 ASVQSKRRKRLRYVYHCTNTDNPYKRGDLTYA INLHNVYKYLRLPYPSNKOVDKYL 480
DB 470 ASVQSKRRKRLRYVYHCTNTDNPYKRGDLTYA INLHNVYKYLRLPYPSNKOVDKYL 529
QY 481 RPLGPHGLSKSVQVQNLGLTLKAVDDQTLPLMEKPLRGSSLGIPAFSYSPFYIRNAKVA 540
DB 530 RPLGPHGLSKSVQVQNLGLTLKAVDDQTLPLMEKPLRGSSLGIPAFSYSPFYIRNAKVA 589
QY 541 ACT 543
DB 590 ACT 592

RESULT 13
ADL6383
ID ADL6383 standard; protein; 592 AA.
XX
AC ADL6383;
DT 06-MAY-2004 (first entry)
XX
DE Human heparanase full length protein.
XX
KW Human, heparanase; heparanase-dependent cancer; cancer;
KW autoimmune reaction; inflammation; chromosome 4; enzyme.
OS
XX Homo sapiens.
PN US2003236215-A1.
XX
PD 25-DEC-2003.
XX
PF 09-JUN-2003; 2003US-00456573.
XX
PR 31-AUG-1998; 98MO-US017954.
PR 01-MAR-1999; 99US-00258892.
PR 08-NOV-1999; 99US-00435739.
XX
PA (INST-) INSTIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASTI MEDICAL RES SERVICES & DEV.
PI Pecker I, Vlodavsky I, Feinstein E;
XX
DR WPI; 2004-070610/07.
XX
PT New antisense oligonucleotide hybridizable with a polynucleotide encoding
PT a polypeptide with heparanase activity, useful for treating diseases such
PT as cancer and autoimmune disorders.
XX
PS Claim 3; SEQ ID NO 14; 108bp; English.
XX
XX
XX The invention relates to an antisense oligonucleotide (ASO) comprising a
XX polynucleotide or a polynucleotide analogue of at least 10 bases being
XX hybridizable in vivo, under physiological conditions, with a portion of
XX a polynucleotide strand encoding a polypeptide having heparanase
XX catalytic activity. Also included are a method of in vivo downregulating
XX heparanase activity (comprising administering the ASO in vivo), a method
XX (characterised by heparanase activity, comprising administering ASO to
XX the subject), a pharmaceutical composition comprising the ASO and a
XX carrier, an antisense nucleic acid construct (comprising the ASO and a
XX sequence and a polynucleotide sequence directing the synthesis of an
XX antisense RNA sequence of at least 10 bases being hybridizable in vivo,
XX under physiological conditions, with a polynucleotide strand encoding a
XX polypeptide having heparanase catalytic activity), a method of in vivo
XX downregulating heparanase activity (comprising administering in vivo the
XX antisense nucleic acid construct), a pharmaceutical composition
XX comprising the antisense nucleic acid construct and a carrier, and an
XX antisense oligonucleotide comprising a polynucleotide or a polynucleotide

CC analogue of at least 10 bases being hybridizable in vivo, under
CC physiological conditions, with a portion of a polynucleotide strand being
CC characterised by forming at least a portion of an untranslated region
CC (UTR) for a polynucleotide strand encoding a polypeptide having
CC heparanase catalytic activity. The methods and compositions of the
CC present invention are useful for the prevention and/or treatment of
CC diseases or conditions associated with aberrant heparanase activity, such
CC as heparanase-dependent cancer, cancer, autoimmune reaction and
CC inflammation. The gene for human heparanase is located on chromosome 4.
CC The present sequence is a human heparanase protein.
SQ Sequence 592 AA;

Query Match 100.0%; Score 2842; DB 8; Length 592;
Best Local Similarity 100.0%; Pred. No. 2.9e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVVDLPFTQEPHLVSPFLSYT 60
DB 50 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVVDLPFTQEPHLVSPFLSYT 109
QY 61 IDAMLATDPRFLLILGSPKRLTLARGISPAVYLRFGTKTDFLIPDKKSTFEERSYMQS 120
DB 110 IDAMLATDPRFLLILGSPKRLTLARGISPAVYLRFGTKTDFLIPDKKSTFEERSYMQS 169
QY 121 QVNODICKYGSIPDVEEKLRLMPYQEOQLLREHYQKKSTYSRSSVDVLYTFANCS 180
DB 170 QVNODICKYGSIPDVEEKLRLMPYQEOQLLREHYQKKSTYSRSSVDVLYTFANCS 229
QY 181 GLDLIFGLNALLTALQWNSNAQILLDYCSSKYNISWEIGNPNPSFLKKAIDFINGS 240
DB 230 GLDLIFGLNALLTALQWNSNAQILLDYCSSKYNISWEIGNPNPSFLKKAIDFINGS 289
QY 241 QLGEDYIQHLKLRKSTFNAKLYGPDVGQPRRTAKLKSFLKAGGVINDSYMHNYL 300
DB 290 QLGEDYIQHLKLRKSTFNAKLYGPDVGQPRRTAKLKSFLKAGGVINDSYMHNYL 349
QY 301 NGRTATREDPLNDPLDIFISSVQVQVFPVVESTPRGKVMWLGETSASVAGGAPLLSDTFA 360
DB 350 NGRTATREDPLNDPLDIFISSVQVQVFPVVESTPRGKVMWLGETSASVAGGAPLLSDTFA 409
QY 361 AGFMWLDKLGASARMGIEVVRQVFFGAGNHYLVNDENPDLDPDWLSLFFPKLVGTXYLM 420
DB 410 AGFMWLDKLGASARMGIEVVRQVFFGAGNHYLVNDENPDLDPDWLSLFFPKLVGTXYLM 469
QY 421 ASVQSKRRKRLRYVYHCTNTDNPYKRGDLTYA INLHNVYKYLRLPYPSNKOVDKYL 480
DB 470 ASVQSKRRKRLRYVYHCTNTDNPYKRGDLTYA INLHNVYKYLRLPYPSNKOVDKYL 529
QY 481 RPLGPHGLSKSVQVQNLGLTLKAVDDQTLPLMEKPLRGSSLGIPAFSYSPFYIRNAKVA 540
DB 530 RPLGPHGLSKSVQVQNLGLTLKAVDDQTLPLMEKPLRGSSLGIPAFSYSPFYIRNAKVA 589
QY 541 ACT 543
DB 590 ACT 592

RESULT 14
ADM48720
ID ADM48720 standard; protein; 592 AA.
XX
AC ADM48720;
DT 03-JUN-2004 (first entry)
XX
DE Human SK-hepl hpa protein.
XX
KW Transgenic animal; heparanase; cancer; viral infection; restenosis;
KW neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;
KW human.
OS Homo sapiens.

```

XX  US2003217375-A1.
PN
XX
PD  20-NOV-2003.
XX
PF  24-FEB-2003; 2003US-00371218.
XX
PR  31-AUG-1998; 98MO-US017954.
PR  01-MAR-1999; 99US-00258892.
PR  06-FEB-2001; 2001US-00776874.
PR  19-NOV-2001; 2001US-00988113.
XX
PA  (ZCHARA/) ZCHARIA E.
PA  (VIOD/) VIODAVSKY I.
PA  (METZ/) METZGER S.
PA  (PECK/) PECKER I.
PA  (ILAN/) ILAN N.
PA  (CHAJ/) CHAJER-SHAUL T.
PA  (GOLD/) GOLDSHMIDT O.
XX
PI  Zcharia E. Viodavsky I., Metzger S., Pecker I., Ilan N.;
PI  Chajek-Shaul T., Goldshmidt O.;
DR  WPI; 2004-021918/02.
DR  N-Psdb; ADM48719, ADM48721.
XX
PT  New transgenic non-human animal expressing heparinase, useful as models
PT  for human disease, such as cancers, viral infection, neurodegenerative
PT  diseases, restenosis, atherosclerosis and pulmonary disorders.
XX
PS  Example 6; SEQ ID NO 14; 106pp; English.
XX
CC  The present invention relates to a transgenic non-human animal whose
CC  genome comprises an exogenous polynucleotide sequence, including a
CC  promoter active in tissues of the non-human, a region encoding a human
CC  heparinase, where the promoter and the region encoding human heparinase
CC  are operably linked in the exogenous polynucleotide such that human
CC  heparinase is expressed in at least a portion of the cells of the non-
CC  human animal. The methods and compositions of the present invention are
CC  useful for the production of transgenic animals expressing heparinase, to
CC  be used as models for human diseases such as cancers, viral infection,
CC  restenosis, neurodegenerative diseases, atherosclerosis and pulmonary
CC  disorders. The present sequence is human SK-hep1 hpa protein used in the
CC  exemplification of the invention.
XX
SQ  Sequence 592 AA;
Query Match 100.0%; Score 2842; DB 8; Length 592;
Beat Local Similarity 100.0%; Pred. No. 2.9e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLNSKRALPPPLMLLLGPIGPIPSGALPRPAQADVDVDDFTFOEPLHLVSPGFLSVT 60
DB 50 MLNSKRALPPPLMLLLGPIGPIPSGALPRPAQADVDVDDFTFOEPLHLVSPGFLSVT 109
QY 61 IDANATPBRPILIGSPKRTIARGLSPAYRFGCTTDPILIPPKKSTFEERSYQOS 120
DB 110 IDANATPBRPILIGSPKRTIARGLSPAYRFGCTTDPILIPPKKSTFEERSYQOS 169
QY 121 QVNODICRYGSIIPVEEKLRLLEMPYQEQOLLREHYOKKFKNSTYSRSVDVLYTFANCS 180
DB 170 QVNODICRYGSIIPVEEKLRLLEMPYQEQOLLREHYOKKFKNSTYSRSVDVLYTFANCS 229
QY 181 GLDLIFGNALRLRTADLQWNSNAQLLDYSSSKQYINISWELGNEPNSFLKKADIFINGS 240
DB 230 GLDLIFGNALRLRTADLQWNSNAQLLDYSSSKQYINISWELGNEPNSFLKKADIFINGS 289
QY 241 QLGEBYIOLHLKLRSTFKNAKLVGPVDVGQPRKTAUKLSLTKGSGVIVSVTHNYL 300
DB 290 QLGEBYIOLHLKLRSTFKNAKLVGPVDVGQPRKTAUKLSLTKGSGVIVSVTHNYL 349
QY 301 NGRTATREDPLNPVDLIFISSVQKVFQVESTPRGKKVWLGETS8AYGGAPLLSDTFA 360

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DB 350 NGRTATREDPLNPVDLIFISSVQKVFQVESTPRGKKVWLGETS8AYGGAPLLSDTFA 409
QY 361 AGFWMLDKLGISARMGIEVWVRQVFGAGNHYLVDENPDPPLPDYMLSLFLFKLVGTXYLM 420
DB 410 AGFWMLDKLGISARMGIEVWVRQVFGAGNHYLVDENPDPPLPDYMLSLFLFKLVGTXYLM 469
QY 421 ASVQSKRRKRLRVYLHCTNTDNPVYKSGDLTLVAIINLHNTKYRLPLPYPSNKKVDXYL 480
DB 470 ASVQSKRRKRLRVYLHCTNTDNPVYKSGDLTLVAIINLHNTKYRLPLPYPSNKKVDXYL 529
QY 481 RPLGPHGLSKSVQNLGTLTKMVDQTLPLMEKPLRPGSGLGIPARSYSFFVIRNAKVA 540
DB 530 RPLGPHGLSKSVQNLGTLTKMVDQTLPLMEKPLRPGSGLGIPARSYSFFVIRNAKVA 589
QY 541 ACI 543
DB 590 ACI 592
RESULT 15
AA17082
ID AA17082 standard; protein; 543 AA.
XX
AC AA17082;
XX
DT 21-JUL-1999 (first entry)
XX
DE Human heparinase enzyme.
XX
KW Heparinase; endoglucuronidase; heparan sulfate proteoglycan; enzyme;
KW metastasis; angiogenesis; wound healing; angioplasty-induced restenosis;
KW atherosclerosis; atherosclerosis; inflammation; tissue development;
KW human; HSPG.
XX
KM Homo sapiens.
XX
PN MO9921975-A1.
XX
PD 06-MAY-1999.
XX
PE 28-OCT-1998; 98MO-AU000898.
XX
PR 28-OCT-1997; 97AU-0000062.
PR 09-DEC-1997; 97AU-00000812.
XX
PA (AUSU ) UNIV AUSTRALIAN NAT.
XX
PI Freeman CG, Hulett MD, Parish CR, Hamdorf BJ;
PI WPI; 1999-312956/26.
XX
DR N-Psdb; AAX37259.
XX
PT Polynucleotides encoding mammalian endoglucuronidases, especially
PT heparinases, useful to promote wound healing.
XX
PS Claim 6; Page 69-73; 112pp; English.
XX
CC The invention relates to nucleic acid sequences that encode heparinase
CC enzymes having endoglucuronidase activity. Recombinant heparinases are
CC capable of removing the HS side chain from heparan sulfate proteoglycan
CC (HSPG). Sulfated oligosaccharides, sulphates or HSPG can be used to
CC inhibit heparinase, this is useful for treatment of a physiological or
CC medical condition associated with elevated heparinase activity such as
CC metastasis, angiogenesis, wound healing, angioplasty-induced restenosis,
CC atherosclerosis, atherosclerosis and inflammation. The human, murine and
CC rat heparinases can be used to enhance wound healing, especially
CC associated with tissue development and repair. The conditions mentioned
CC above can be diagnosed using specific antibodies, and also using primers
CC and probes specific for the heparinase polynucleotides. Other uses of the
CC heparinases include sequencing sulfated molecules such as HSPG. The
CC present sequence represents a human heparinase
SQ Sequence 543 AA;

```

Query Match 99.9%; Score 2838; DB 2; Length 543;
 Best Local Similarity 99.8%; Pred. No. 6.2e-273;
 Matches 542; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MLRSKRALPPMLLLGLPLSPGALPRPAQADVDLDFEFOEPLHVSPLSVT 60
Db      1 MLRSKRALPPMLLLGLPLSPGALPRPAQADVDLDFEFOEPLHVSPLSVT 60
QY      61 IDANLATDPRFLILGSPKRLTARGLSPAYIRFGGTYTDFLIPDPKKESTFEERSYWG 120
Db      61 IDANLATDPRFLILGSPKRLTARGLSPAYIRFGGTYTDFLIPDPKKESTFEERSYWG 120
QY      121 QVNODICKYGSIPPDVEEKLRLMPYOBQLLRHYOKKPKNSTYSSSDVLYTFPANGS 180
Db      121 QVNODICKYGSIPPDVEEKLRLMPYOBQLLRHYOKKPKNSTYSSSDVLYTFPANGS 180
QY      181 GLDLIFGINALLRTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFING 240
Db      181 GLDLIFGINALLRTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFING 240
QY      241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGOPRRRTAKMLKSLKAGGEVIDSVTHHYLL 300
Db      241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGOPRRRTAKMLKSLKAGGEVIDSVTHHYLL 300
QY      301 NGRTATREDPLNPDVLDIFISSVQKVFQVVESTRPGKWLGETSSAYGGAPLSDTPA 360
Db      301 NGRTATREDPLNPDVLDIFISSVQKVFQVVESTRPGKWLGETSSAYGGAPLSDTPA 360
QY      361 AGFWMLDKLGLSARMGIEVVMROVFGAGNYHLVDENPDLPDYLSTLFFKLVGTXYLM 420
Db      361 AGFWMLDKLGLSARMGIEVVMROVFGAGNYHLVDENPDLPDYLSTLFFKLVGTXYLM 420
QY      421 ASVOGSKRRRLRYLHCTNTDNPYKSGDLYLVAIINAVTKYRLPYPFSSKQVDKYL 480
Db      421 ASVOGSKRRRLRYLHCTNTDNPYKSGDLYLVAIINAVTKYRLPYPFSSKQVDKYL 480
QY      481 RPLGPHGLLSKSYQNLGLTLKQVDDQTLPLMEKPLRPSSSLGLPAFSYSFFVIRNAKVA 540
Db      481 RPLGPHGLLSKSYQNLGLTLKQVDDQTLPLMEKPLRPSSSLGLPAFSYSFFVIRNAKVA 540
QY      541 ACT 543
Db      541 ACT 543

```

Search completed: February 28, 2005, 05:56:40
 Job time : 176 secs


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Db 241 CCAATGACGCCAACCTGGCCACGACCCGCGTTCTCTCATCTCTCTGTTCTCCAAAGC 300
Qy 301 TTGGAACCTGGCCAGAGGCTTGTCTCTCTGCTAAGGCTTGTGGCACCAGACAG 360
Db 301 TTGGAACCTGGCCAGAGGCTTGTCTCTCTGCTAAGGCTTGTGGCACCAGACAG 360
Qy 361 ACTTCTAATTTTGCATCCCAAGAGATCAACCTTGAAGAGAGAGTTACTGGCAAT 420
Db 361 ACTTCTAATTTTGCATCCCAAGAGATCAACCTTGAAGAGAGAGTTACTGGCAAT 420
Qy 421 CTGAAGTCAACCAAGATTTTGCATATGATTCATCCCTCTGATGTGAGAGAGAT 480
Db 421 CTGAAGTCAACCAAGATTTTGCATATGATTCATCCCTCTGATGTGAGAGAGAT 480
Qy 481 TAAGTTGGAATGGCCCTTACCAAGAGATGCTACTCTGAGAGACCTACCGAAAAAGT 540
Db 481 TAAGTTGGAATGGCCCTTACCAAGAGATGCTACTCTGAGAGACCTACCGAAAAAGT 540
Qy 541 TCAAGAACAGACCTTACTCAAGAGCTCTGATAGTGTATACATTTTGGCAACTGCT 600
Db 541 TCAAGAACAGACCTTACTCAAGAGCTCTGATAGTGTATACATTTTGGCAACTGCT 600
Qy 601 CAGAGCTGACCTGATCTTGGCTTAATGCGTTATTAAGAACAGCAATTTGACGTGA 660
Db 601 CAGAGCTGACCTGATCTTGGCTTAATGCGTTATTAAGAACAGCAATTTGACGTGA 660
Qy 661 ACAGTTCTAATGCTAGTTGCTCTGAGACTAATGCTTAATGAACACAGATTTGACGTGA 720
Db 661 ACAGTTCTAATGCTAGTTGCTCTGAGACTAATGCTTAATGAACACAGATTTGACGTGA 720
Qy 721 GGAACCTAGCAATGAACCTAAGTTCTTAAAGAGGCTGATATTTTCAATCAATGGGT 780
Db 721 GGAACCTAGCAATGAACCTAAGTTCTTAAAGAGGCTGATATTTTCAATCAATGGGT 780
Qy 781 GCGAGTTAGAGAGATTAATTCATATGCAATTAATCTTAAGAAAGTCCCTTCAAAA 840
Db 781 GCGAGTTAGAGAGATTAATTCATATGCAATTAATCTTAAGAAAGTCCCTTCAAAA 840
Qy 841 ATGCAAACTCTAATGCTCTGATGTTGCTGAGCTCGAAGAGAGAGCGCTAAGATGCTGA 900
Db 841 ATGCAAACTCTAATGCTCTGATGTTGCTGAGCTCGAAGAGAGAGCGCTAAGATGCTGA 900
Qy 901 AGAGCTTCTGAAGGCTGAGAGAGATGATGATTAAGTACATGAGTCACTACTAAT 960
Db 901 AGAGCTTCTGAAGGCTGAGAGAGATGATGATTAAGTACATGAGTCACTACTAAT 960
Qy 961 TGAATGACGCACTGCTACAGGAGATTTTCAAACTCTGATGATGATGATGATTTTA 1020
Db 961 TGAATGACGCACTGCTACAGGAGATTTTCAAACTCTGATGATGATGATGATTTTA 1020
Qy 1021 TTTGATCTGTGCAAAAAGTTTCCAGGTGTTGAGAGACACAGGCTGAGAGAGATTTTA 1080
Db 1021 TTTGATCTGTGCAAAAAGTTTCCAGGTGTTGAGAGACACAGGCTGAGAGAGATTTTA 1080
Qy 1081 GGTGAGAGAAACAAGCTCTGCAATGAGAGGCGGAGCGCTTGTATCCGACACCTTTG 1140
Db 1081 GGTGAGAGAAACAAGCTCTGCAATGAGAGGCGGAGCGCTTGTATCCGACACCTTTG 1140
Qy 1141 CAGTGGCTTATGCTGAGATTAATGAGGCTCTGAGCGGAGATGAGATGAGATGAG 1200
Db 1141 CAGTGGCTTATGCTGAGATTAATGAGGCTCTGAGCGGAGATGAGATGAGATGAG 1200
Qy 1201 TGAATGAGCAAGATTTCTTGGAGAGAGAACTACATTTAGTGAATGAGAACTTCGATC 1260
Db 1201 TGAATGAGCAAGATTTCTTGGAGAGAGAACTACATTTAGTGAATGAGAACTTCGATC 1260
Qy 1261 CTTTACCTAATTTGGCTATCTCTTCAAGAAATGAGTGGGCAACAGGTGTTAA 1320
Db 1261 CTTTACCTAATTTGGCTATCTCTTCAAGAAATGAGTGGGCAACAGGTGTTAA 1320
Qy 1321 TGGCAGCGTGAAGGTTCAAGAGAGAGAGCTTGATTAATCTTCAATGACACAAACA 1380
Db 1321 TGGCAGCGTGAAGGTTCAAGAGAGAGAGCTTGATTAATCTTCAATGACACAAACA 1380

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Db 1321 TGGCAGCGTGAAGGTTCAAGAGAGAGAGCTTGATTAATCTTCAATGACACAAACA 1380
Qy 1381 CTGCAATCCCAAGATTAAGAGAGAGATTTACTCTGATAGCCATTAACCTCATACG 1440
Db 1381 CTGCAATCCCAAGATTAAGAGAGAGATTTACTCTGATAGCCATTAACCTCATACG 1440
Qy 1441 TCACCAAGTACTGCGGTACCTCTATCTTTTCTAACAAGAGAGATTAATACCTTC 1500
Db 1441 TCACCAAGTACTGCGGTACCTCTATCTTTTCTAACAAGAGAGATTAATACCTTC 1500
Qy 1501 TAAACCTTTTGGAGCTCATGATTTAATTCTTCAAAATCTGCAACTCAATGCTTAATC 1560
Db 1501 TAAACCTTTTGGAGCTCATGATTTAATTCTTCAAAATCTGCAACTCAATGCTTAATC 1560
Qy 1561 TAAAGATGAGTGAATCAAACTTGCACCTTAAATGAGAAAACTCTCCGCGCAGAA 1620
Db 1561 TAAAGATGAGTGAATCAAACTTGCACCTTAAATGAGAAAACTCTCCGCGCAGAA 1620
Qy 1621 GTTCACTGGGCTTGCAGCTTCTCATATATGTTTTTGTGATTAAGAAATGCCAAAGTTG 1680
Db 1621 GTTCACTGGGCTTGCAGCTTCTCATATATGTTTTTGTGATTAAGAAATGCCAAAGTTG 1680
Qy 1681 CTGCTTGCATCTGAATAATTAATATATAGTCTGACTGACTG 1721
Db 1681 CTGCTTGCATCTGAATAATTAATATATAGTCTGACTGACTG 1721

RESULT 2
AR080680 1721 bp DNA linear PAT 31-AUG-2000
LOCUS AR080680
DEFINITION Sequence 11 from patent US 5968822.
ACCESSION AR080680
VERSION AR080680.1 GI:10007410
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1721)
AUTHORS Pecker, I., Violdavsky, I. and Feinstein, E.
TITLE Polynucleotide encoding a polypeptide having heparanase activity
JOURNAL and expression of same in transduced cells
FEATURES
source Location/Qualifiers
1..1721
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 1721; DB 6; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAAGCTTTTGCATCTTCCGCTGCGGCGAGCTGGCGGGGAGAGACGAGTGAACCA 60
Db 1 CTAAGCTTTTGCATCTTCCGCTGCGGCGAGCTGGCGGGGAGAGAGCGAGTGAACCA 60
Qy 61 AGATGCTGCTGCGCTGCAAGCTGCGGCTGCGCGCGCGCGCTGATAGCTGCTCTGGGCG 120
Db 61 AGATGCTGCTGCGCTGCAAGCTGCGGCTGCGCGCGCGCGCTGATAGCTGCTCTGGGCG 120
Qy 121 CGCTGGGTCCCTCTCTCCCTGCGGCGCTGCGCGAGCTGCGAGAGACAGAGAGTGTGG 180
Db 121 CGCTGGGTCCCTCTCTCCCTGCGGCGCTGCGCGAGCTGCGAGAGACAGAGAGTGTGG 180
Qy 181 ACCTGACCTTCTTACCCAGAGAGCGCTGCACTGATGAGCCCTGCTGCTGCTGCTCA 240
Db 181 ACCTGACCTTCTTACCCAGAGAGCGCTGCACTGATGAGCCCTGCTGCTGCTGCTCA 240
Qy 241 CCAATTAGCGCAACCTGGCAGAGACCGCGGTTCTCTCATCTCTGAGTTCTCCAAAGC 300
Db 241 CCAATTAGCGCAACCTGGCAGAGACCGCGGTTCTCTCATCTCTGAGTTCTCCAAAGC 300
Qy 301 TTGTAACCTTGGGCGCAGAGGCTTGTCTCTGCGTACCTGAGGTTTGGTGGCAACAGACG 360

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Db      |||
301  TTGCACTTGGCCAGAGGCTGTCTCTCGTACTGAGGTTGGTGGCAACAAGACAG 360
Qy      |||
361  ACTTCCTAATTTTGGATCCCAAGAAATCAACCTTTGAAGAAGAAGTAACTGGCAAT 420
Db      |||
361  ACTTCCTAATTTTGGATCCCAAGAAATCAACCTTTGAAGAAGAAGTAACTGGCAAT 420
Qy      |||
421  CTCAAGTCAACCAAGATATTGGCAAAATATGGATCCATCCCTCTGATGGAGGAGAGT 480
Db      |||
421  CTCAAGTCAACCAAGATATTGGCAAAATATGGATCCATCCCTCTGATGGAGGAGAGT 480
Qy      |||
481  TACGGTTGAATGGCCCTTACCAAGAGCAATTTGCTAATCCGAAACACTACCAAGAAAAGT 540
Db      |||
481  TACGGTTGAATGGCCCTTACCAAGAGCAATTTGCTAATCCGAAACACTACCAAGAAAAGT 540
Qy      |||
541  TCAAGAACAGCACTTACTCAAGAAAGCTCTGTAGATGTCTATACATTTTGGCAAACTGCT 600
Db      |||
541  TCAAGAACAGCACTTACTCAAGAAAGCTCTGTAGATGTCTATACATTTTGGCAAACTGCT 600
Qy      |||
601  CAGGACTGGACTTGTATCTTGGCCCTAAATGGGTTATTAAAGACAGCAGATTTGGCAGTGA 660
Db      |||
601  CAGGACTGGACTTGTATCTTGGCCCTAAATGGGTTATTAAAGACAGCAGATTTGGCAGTGA 660
Qy      |||
661  ACAGTTCTAATGCTCAAGTTCCTCTGGACTAATGCTCTCTCAAGGGGATTAACAATTTCTT 720
Db      |||
661  ACAGTTCTAATGCTCAAGTTCCTCTGGACTAATGCTCTCTCAAGGGGATTAACAATTTCTT 720
Qy      |||
721  GGGAACTGAGCAATGAACCTTAACAGTTCTTTAAAGAGGCTGATTTTTCATCAATGGGT 780
Db      |||
721  GGGAACTGAGCAATGAACCTTAACAGTTCTTTAAAGAGGCTGATTTTTCATCAATGGGT 780
Qy      |||
781  CGCAGTTAGAGAGATTAATATCAATGATCAATTAAGTCTTAAGAAAGTCCACTTCAAAA 840
Db      |||
781  CGCAGTTAGAGAGATTAATATCAATGATCAATTAAGTCTTAAGAAAGTCCACTTCAAAA 840
Qy      |||
841  ATGCAGAACTCTATGCTCTGATGTGTGTCAGCCTCGAAGAAAGACGCTAAGATGCTGA 900
Db      |||
841  ATGCAGAACTCTATGCTCTGATGTGTGTCAGCCTCGAAGAAAGACGCTAAGATGCTGA 900
Qy      |||
901  AGAGCTTCTTAAGGCTGTGTGAGAGAGATTTGATTCAGTTCACTGATCACTAATCTT 960
Db      |||
901  AGAGCTTCTTAAGGCTGTGTGAGAGAGATTTGATTCAGTTCACTGATCACTAATCTT 960
Qy      |||
961  TGAATGAGCGAGCTGTCTACAGGGAAGATTTTCTAACCCTGATGTATTTGCAATTTT 1020
Db      |||
961  TGAATGAGCGAGCTGTCTACAGGGAAGATTTTCTAACCCTGATGTATTTGCAATTTT 1020
Qy      |||
1021  TTTGATCTGTGCAAAAATTTTTCAGGTGTGAGAGACACAGGCTGGCAAGAGTCT 1080
Db      |||
1021  TTTGATCTGTGCAAAAATTTTTCAGGTGTGAGAGACACAGGCTGGCAAGAGTCT 1080
Qy      |||
1081  GGTTAGAGAAACAAGCTCTGATATGAGAGCGGAGCCCTTGTCTATCCACACCTTTG 1140
Db      |||
1081  GGTTAGAGAAACAAGCTCTGATATGAGAGCGGAGCCCTTGTCTATCCACACCTTTG 1140
Qy      |||
1141  CAGGCTGCTTATGCTGTGATAAATGGGCTGTACGCCGAAATGGGAAATAGAAGTGG 1200
Db      |||
1141  CAGGCTGCTTATGCTGTGATAAATGGGCTGTACGCCGAAATGGGAAATAGAAGTGG 1200
Qy      |||
1201  TGAATGAGCAAGATTTCTTTGAGAGCAGAAAATCAATTTAGTGAATGAGATTTGATC 1260
Db      |||
1201  TGAATGAGCAAGATTTCTTTGAGAGCAGAAAATCAATTTAGTGAATGAGATTTGATC 1260
Qy      |||
1261  CTTTAACTGATTAATTTGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGCAACAAGTGT 1320
Db      |||
1261  CTTTAACTGATTAATTTGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGCAACAAGTGT 1320
Qy      |||
1321  TGGCAAGGCTGCAAGGTTCAAGAGAGAGAGCTTCAAGTATACCTTATTTGCAACAACA 1380
Db      |||
1321  TGGCAAGGCTGCAAGGTTCAAGAGAGAGAGCTTCAAGTATACCTTATTTGCAACAACA 1380
Qy      |||
1381  CTGCAATCCAAAGTATTAAGAGAGATTTAACTCTGTATGCCATTAACCTCCATTAACG 1440

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Db      |||
1381  CTGCAATCCAAAGTATTAAGAGAGATTTAACTCTGTATGCCATTAACCTCCATTAACG 1440
Qy      |||
1441  TCACCAAGTATTTGGGTTACCCATCTTTTCTAACAAGCAAGTGAATTAATACCTTC 1500
Db      |||
1441  TCACCAAGTATTTGGGTTACCCATCTTTTCTAACAAGCAAGTGAATTAATACCTTC 1500
Qy      |||
1501  TAAAGCTTTGGGACCTCATGATTAATCTTCAAAATCTGTCCAATGATGTAACTTC 1560
Db      |||
1501  TAAAGCTTTGGGACCTCATGATTAATCTTCAAAATCTGTCCAATGATGTAACTTC 1560
Qy      |||
1561  TAAAGATGTGATGATCAAACTTCCACCTTTAATGAGAAAACCTCTCCGGCAGAGAA 1620
Db      |||
1561  TAAAGATGTGATGATCAAACTTCCACCTTTAATGAGAAAACCTCTCCGGCAGAGAA 1620
Qy      |||
1621  GTTCACTGGGCTTGCAGCTTTTCTCATATAGTTTGTGATTAAGAAATGCCAAAGTTG 1680
Db      |||
1621  GTTCACTGGGCTTGCAGCTTTTCTCATATAGTTTGTGATTAAGAAATGCCAAAGTTG 1680
Qy      |||
1681  CTGCTGATCTGAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1721
Db      |||
1681  CTGCTGATCTGAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1721

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RESULT 3
LOCUS AR125603 1721 bp. DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6177545.
ACCESSION AR125603
VERSION AR125603.1 GI:14111665
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1721)
AUTHORS Pecker, I., Vlodevsky, I., Friedman, Y. and Peretz, T.
TITLE Hepatoma-specific molecular probes and their use in research and medical applications
JOURNAL Patent: US 6177545-A 1 23-JAN-2001;
FEATURES location/Qualifiers
1..1721
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 1721; DB 6; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      |||
1  CTAGAGCTTTGCACTCTCCGCTGCGCGAGCTGGCGGGGAGACAGCAGGTGAGCCCA 60
Db      |||
1  CTAGAGCTTTGCACTCTCCGCTGCGCGAGCTGGCGGGGAGACAGCAGGTGAGCCCA 60
Qy      |||
61  AGATGCTGCTGCGCTCGAAGCTTCCGCTGCGCGCGCGCTGATCTGCTCTGGGGC 120
Db      |||
61  AGATGCTGCTGCGCTCGAAGCTTCCGCTGCGCGCGCGCTGATCTGCTCTGGGGC 120
Qy      |||
121  CGCTGGATCCCTCTCCCTGGGCGCGCTGGCCGACCTGGGCAAGACAGGACGATCGTG 180
Db      |||
121  CGCTGGATCCCTCTCCCTGGGCGCGCTGGCCGACCTGGGCAAGACAGGACGATCGTG 180
Qy      |||
181  ACTGGAATCTTTCACCCAGAGCGGTGCACTGTGATGAGCCCTGTTCTGTCTGCTCA 240
Db      |||
181  ACTGGAATCTTTCACCCAGAGCGGTGCACTGTGATGAGCCCTGTTCTGTCTGCTCA 240
Qy      |||
241  CCATTGAGCCCACTGGGCGCAGGACCGCGGTTCTCTATCTCTGGGTTCTCAAAAGC 300
Db      |||
241  CCATTGAGCCCACTGGGCGCAGGACCGCGGTTCTCTATCTCTGGGTTCTCAAAAGC 300
Qy      |||
301  TTGTAACCTTTGGGCGAGAGGCTTGTCTCTGCTGCTAAGGTTTGGTGGCAACAAGCAG 360
Db      |||
301  TTGTAACCTTTGGGCGAGAGGCTTGTCTCTGCTGCTAAGGTTTGGTGGCAACAAGCAG 360
Qy      |||
361  ACTTCTAATTTTGCATCCCAAGAGATCAACCTTTGAAGAGAGATTAATCTGGCAAT 420

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Db      361  ACTTCCTAATTTTGGATCCCAAGAGAAATCAACTTTGAGAGAGAGTACTGGCAAT 420
Qy      421  CTGAAGCAACCGAGATATTGGAAATAGATCCATCCCTCTGATGTGGAGAGAGT 480
Db      421  CTGAAGCAACCGAGATATTGGAAATAGATCCATCCCTCTGATGTGGAGAGAGT 480
Qy      481  TACGGTTGAAATGGCCCTACCAAGAGAAATGTCTACCTCCGAGAGACCTACCGAAAAAT 540
Db      481  TACGGTTGAAATGGCCCTACCAAGAGAAATGTCTACCTCCGAGAGACCTACCGAAAAAT 540
Qy      541  TCAGAAACAGCACTACTCAAGAAAGCTGTAGATGTCTATACATTTTGGAAAACTGCT 600
Db      541  TCAGAAACAGCACTACTCAAGAAAGCTGTAGATGTCTATACATTTTGGAAAACTGCT 600
Qy      601  CAGGACTGACCTGATCTTTGGCTTAATGCGTTAATAGCAAGACAGCAATTTGCACTGTA 660
Db      601  CAGGACTGACCTGATCTTTGGCTTAATGCGTTAATAGCAAGACAGCAATTTGCACTGTA 660
Qy      661  ACAGTTCTAATGTCTAGTTGCTCTGGACTACTGCTCTTCAAGGGGATTAACATTTCTT 720
Db      661  ACAGTTCTAATGTCTAGTTGCTCTGGACTACTGCTCTTCAAGGGGATTAACATTTCTT 720
Qy      721  GGGAACTAGCAATGAACCTAACATTTCTTAAGAGGCTGATATTTTCATCAATGGGT 780
Db      721  GGGAACTAGCAATGAACCTAACATTTCTTAAGAGGCTGATATTTTCATCAATGGGT 780
Qy      781  CGCAGTTAGAGAAATTAATTAATTCATTAATGATTAATTAATTAATTAATTAATTAAT 840
Db      781  CGCAGTTAGAGAAATTAATTAATTCATTAATGATTAATTAATTAATTAATTAATTAAT 840
Qy      841  ATGCAAAATCTATAGTCTCTGATGTTGCTGAGCTCGAAGAAAGACGGCTAAGATGCTGA 900
Db      841  ATGCAAAATCTATAGTCTCTGATGTTGCTGAGCTCGAAGAAAGACGGCTAAGATGCTGA 900
Qy      901  AGAGCTTCTGAAGGCTGATGAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAAT 960
Db      901  AGAGCTTCTGAAGGCTGATGAGAAAGATTAATTAATTAATTAATTAATTAATTAATTAAT 960
Qy      961  TGAATGACCGACCTGCTACCAAGGAAAGATTTTCAAAACCTGATGATTTGGACATTTTGA 1020
Db      961  TGAATGACCGACCTGCTACCAAGGAAAGATTTTCAAAACCTGATGATTTGGACATTTTGA 1020
Qy      1021  TTTCACTGTCGCAAAAGATTTTCAAGGCTGATGAGACCAAGGCTGCGCAAGAGGCTCT 1080
Db      1021  TTTCACTGTCGCAAAAGATTTTCAAGGCTGATGAGACCAAGGCTGCGCAAGAGGCTCT 1080
Qy      1081  GGTAGAGAAACAAGCTCTGATATGAGAGCGAGCGCCCTTGTCTATCCGACACCTTTG 1140
Db      1081  GGTAGAGAAACAAGCTCTGATATGAGAGCGAGCGCCCTTGTCTATCCGACACCTTTG 1140
Qy      1141  CAGCTGGCTTAAATGCTGATTAATTTGGCTCTGACGCCCGAATGGAAATGAAATGG 1200
Db      1141  CAGCTGGCTTAAATGCTGATTAATTTGGCTCTGACGCCCGAATGGAAATGAAATGG 1200
Qy      1201  TGAATGAGCAAGATTTTGGAGCAGAAATCACTAATTAATGAGATGAAATCTTGAATC 1260
Db      1201  TGAATGAGCAAGATTTTGGAGCAGAAATCACTAATTAATGAGATGAAATCTTGAATC 1260
Qy      1261  CTTTAACTGATTAATGCTTCTCTGTTCAAGAAATGGTGGGACCAAGAGTTTAA 1320
Db      1261  CTTTAACTGATTAATGCTTCTCTGTTCAAGAAATGGTGGGACCAAGAGTTTAA 1320
Qy      1321  TGGCAAGCGTGAAGGTTCAAGAGAAAGGCTTGAATACCTTCAATTTGACAAACA 1380
Db      1321  TGGCAAGCGTGAAGGTTCAAGAGAAAGGCTTGAATACCTTCAATTTGACAAACA 1380
Qy      1381  CTGACATCCAGAGTTAAAGAGAGATTTAACTGTATGCAATTAACCTCCATACG 1440
Db      1381  CTGACATCCAGAGTTAAAGAGAGATTTAACTGTATGCAATTAACCTCCATACG 1440
Qy      1441  TCACCAAGTACTTGGGTTACCTATCCTTTTCTAAACAAGAGTGAATTAACCTTC 1500

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Db      1441  TCACCAAGTACTTGGGTTACCTATCCTTTTCTAAACAAGAGTGAATTAACCTTC 1500
Qy      1501  TAAAGCCTTTGGGACCTCANTGATTAATTTTCGAATATGTTCGAATCAATGTCTAACTC 1560
Db      1501  TAAAGCCTTTGGGACCTCANTGATTAATTTTCGAATATGTTCGAATCAATGTCTAACTC 1560
Qy      1561  TAAAGATGTGATGATCAAACTTGGCACCTTAAATGAAAACTCTCGGCGCAGAA 1620
Db      1561  TAAAGATGTGATGATCAAACTTGGCACCTTAAATGAAAACTCTCGGCGCAGAA 1620
Qy      1621  GTTCACTGGGCTTGGCAGCTTTCTCATATATGTTTTTTTGTATPAAGAAATGCCAAAGTTG 1680
Db      1621  GTTCACTGGGCTTGGCAGCTTTCTCATATATGTTTTTTTGTATPAAGAAATGCCAAAGTTG 1680
Qy      1681  CTGCTGCATCTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1721
Db      1681  CTGCTGCATCTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1721

RESULT 4
ARI25604      1721 bp      DNA      linear      PAT 16-MAY-2001
LOCUS      AR125604
DEFINITION      Sequence 3 from patent US 6177545.
ACCESSION      AR125604
VERSION      AR125604.1 GI:14111666
KEYWORDS
SOURCE
ORGANISM      Unknown.
REFERENCE      Unpublished.
AUTHORS      1 (bases 1 to 1721)
TITLE      Pecker, I., Vladavsky, I., Friedman, Y. and Perets, T.
JOURNAL      Heparanase specific molecular probes and their use in research and
FEATURES      medical applications
PATent: US 6177545-A 3 23-JAN-2001;
LOCation/Qualifiers
1..1721
source
/mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 1721; DB 6; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1      CTAGAGCTTTGACCTCCGCTGCGCGGACAGTGTGCGGGGAGAGCCAGGTGAGCCCA 60
Db      1      CTAGAGCTTTGACCTCCGCTGCGCGGACAGTGTGCGGGGAGAGCCAGGTGAGCCCA 60
Qy      61  AGATGCTGTGCTGCTGAGAGCTGCGCTGCGCGCGCGCTGATGCTGCTCGGGGCG 120
Db      61  AGATGCTGTGCTGCTGAGAGCTGCGCTGCGCGCGCGCGCTGATGCTGCTCGGGGCG 120
Qy      121  GCGTGGGCTCCCTCTCCCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db      121  GCGTGGGCTCCCTCTCCCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Qy      181  ACTGGAATCTTCTACACCGAGAGCGCGTGAACCTGATGAGCGCGCTCTCTCTGCGCTCA 240
Db      181  ACTGGAATCTTCTACACCGAGAGCGCGTGAACCTGATGAGCGCGCTCTCTCTGCGCTCA 240
Qy      241  CCATTTGACGCAACCTGCGCAACCGAGCGCGGTTCTCATCTCTCTGCGGTTCTCAAGC 300
Db      241  CCATTTGACGCAACCTGCGCAACCGAGCGCGGTTCTCATCTCTCTGCGGTTCTCAAGC 300
Qy      301  TTGGAACCTTGGGCGAGAGGCTGTCTCTGCTGATACCTGAGGTTTGGTGGCAACAAGCAG 360
Db      301  TTGGAACCTTGGGCGAGAGGCTGTCTCTGCTGATACCTGAGGTTTGGTGGCAACAAGCAG 360
Qy      361  ACTTCTAATTTTGGATCCCAAGAGAGATCAACTTTGAAGAGAGAGATTTACTGGCAAT 420
Db      361  ACTTCTAATTTTGGATCCCAAGAGAGATCAACTTTGAAGAGAGAGATTTACTGGCAAT 420
Qy      421  CTGAAGTCAACCAAGATATTGTCAAATATGATTCATCCCTCTGATGTGGAGAGAGAT 480

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[illegible]

Db	1501	TAAAGACCTTTGGGAACCTCAGTGGATTACTTTCCAAATCTGTCCAACTCAATG9TCTAACTC	1560		
QY	1561	TAAAGATGCTGATGATCAAACTTTGCCACCTTTAATGAAAAAACCCTTCGGGCCAGAA	1620		
Db	1561	TAAAGATGATGATGATCAAACTTTGCCACCTTTAATGAAAAAACCCTTCGGGCCAGAA	1620		
QY	1661	GTTACACGGGGCTTGCGACGCTTCTCATATACCTTTTTTTTGGATAGAAATGCCAAAGTTG	1680		
Db	1661	GTTACACGGGGCTTGCGACGCTTCTCATATATATTTTTTTTTTGGATAGAAATGCCAAAGTTG	1680		
QY	1681	CTGCTTGATCTGAAAAATAAATATACTAGTCTGACACTG	1721		
Db	1681	CTGCTTGATCTGAAAAATAAATATACTAGTCTGACACTG	1721		
RESULT 5	BD193236	1721 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD193236				
DEFINITION	Heparanase specific molecular probes and their use in research and medical applications.				
ACCESSION	BD193236				
VERSION	BD193236.1	GI:33002975			
KEYWORDS	JP 2002512533-A/1.				
SOURCE	Streptococcus equi				
ORGANISM	Streptococcus equi				
REFERENCE	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.				
AUTHORS	1 (bases 1 to 1721) Pecker,I., Vlodayvsky,I., Friedman,Y. and Perets,T.				
TITLE	Heparanase specific molecular probes and their use in research and medical applications				
JOURNAL	Patent: JP 2002512533-A 1 23-APR-2002; INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES & DEVELOPMENT LTD				
COMMENT	PN JP 2002512533-A/1 PD 23-APR-2002 PF 29-APR-1999 JP 1999555528 PR 01-MAY-1998 US 09/071739 PI IRIS PECKER, ISRAEL VLADAVSKY, Yael FRIEDMAN, TUVIA PERETS PC C07K16/00,C07K16/40,G01N33/53,C07H21/02,C7H21/04,A61K39/395 CC nucleic acid				
FEATURES	key	Location/Qualifiers.			
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ORIGIN	1..1721	Location/Qualifiers			
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	/mol_type="Genomic DNA"				
	/db_xref="taxon:1336"				
	Query Match	100.0%; Score 1721; DB 6; Length 1721;			
	Best Local Similarity	100.0%; Pred. No. 0;			
	Matches 1721; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1	CTAAGACTTTTGAATCTCCGCTGGCGGCACTGGCGGGGAGACGACAGCTAGACCCA	60		
QY	61	AGATGCTGTCGCTCGAAGCTGCGGCGCGCGCGCTGATGCTGCTCCGAGGGC	120		
Db	61	AGATGCTGTCGCTCGAAGCTGCGGCGCGCGCGCTGATGCTGCTCCGAGGGC	120		
QY	121	CGCTGGGCTCCCTCTCCCTGCGCGCCCTCGACGCTGCGCAAGCAAGAGCGTCTGG	180		
Db	121	CGCTGGGCTCCCTCTCCCTGCGCGCGCCCTCGACGCTGCGCAAGCAAGAGCGTCTGG	180		
QY	181	ACCTGGAATTTCTTACCAAGAGACCGCTGCACTGTGTGAGCCCTCGTTCTGTCCGCA	240		
Db	181	ACCTGGAATTTCTTACCAAGAGACCGCTGCACTGTGTGAGCCCTCGTTCTGTCCGCA	240		
QY	241	CCATTGACGCAACCTGGCCAGGACCGCGAGTTCTCATCTCTCGGATTCTCCAAAGC	300		
Db	241	CCATTGACGCAACCTGGCCAGGACCGCGAGTTCTCATCTCTCGGATTCTCCAAAGC	300		

QY 301 TTGTAACCTTGCCAGAGGCTTGTCTCTGCTACTGAGGTTGTGGACCAAGCAG 360
 Db 301 TTGTAACCTTGCCAGAGGCTTGTCTCTGCTACTGAGGTTGTGGACCAAGCAG 360
 QY 361 ACTTCCTAATTTTGGATCCCAAGAAAGATCACTTTGAAGAGAAAGTTACTGGCAAT 420
 Db 361 ACTTCCTAATTTTGGATCCCAAGAAAGATCACTTTGAAGAGAAAGTTACTGGCAAT 420
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 LOCUS BD193237
 DEFINITION Hepatranase specific molecular probes and their use in research and medical applications.
 ACCESSION BD193237
 VERSION BD193237.1 GI:33002976
 KEYWORDS JP 2002512533-A/2.
 SOURCE Streptococcus equi
 ORGANISM Streptococcus equi
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
 1 (bases 1 to 1721)
 Pecker, I., Vlodavsky, I., Friedman, Y. and Perets, T.
 Hepatranase specific molecular probes and their use in research and medical applications
 Patent: JP 2002512533-A 2 23-APR-2002;
 INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES & DEVELOPMENT LTD
 PN JP 2002512533-A/2
 PD 23-APR-2002
 PR 29-APR-1999 JP 1999555528
 PI IRIS PECKER, ISRAEL, VLODAVSKY, YAEI, FRIEDMAN, TUVIA PERETS PC
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Db	1021	TTTCAATCTGTGCAAAAGTTTTCAGGTGTGTAAGACACAGGCTGTGCAAGAGTCT	1080
Qy	1081	GGTTAGAGAAACAGAGCTGTGATATGAGGCGGAGCGCCCTTGCTATCCGACACTT	1140
Db	1081	GGTTAGAGAAACAGAGCTGTGATATGAGGCGGAGCGCCCTTGCTATCCGACACTT	1140
Qy	1141	CAGCTGCTTATGTGTGATTAATTTGGGCTGTACGCCCCGAATGGGAATAGAAGT	1200
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QY	1381	CTGCAATCCCAAGGTATTAAGAGAGAGATTTTAACTCTGTATGCCATAAACCTCCATAACG	1440	
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DEFINITION				Cells genetically modified for expressing recombinant heparanase
ACCESSION		BD05238		and method, and method of purifying recombinant heparanase.
VERSION		BD05238.1		GI:33015008
KEYWORDS		JP 2002513560-A/1.		
SOURCE		unidentified		
ORGANISM		unclassified.		
REFERENCE		1 (bases 1 to 1721)		
AUTHORS		Artzi,H.B., Hershkovitz,M.A., Zeevi,O.Y., Becker,I., Peleg,Y.,		
TITLE		Shlom,I.Y., Moskowit,H., Miron,D., Gilboa,A. and Mimon,M.		
JOURNAL		Cells genetically modified for expressing recombinant heparanase		
COMMENT		and method, and method of purifying recombinant heparanase		
		Patent: JP 2002513560-A 1 14-MAY-2002;		
		INSIGHT STRATEGY AND MARKETING LTD		
		OS Unidentified		
		PN JP 2002513560-A/1		
		PD 14-MAY-2002		
		PF 29-APR-1999 JP 2000547200		
		PR 01-MAY-1998 US 09/071618, 02-MAR-1999 US 09/260038		
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		PECKER,		
		PI YOAV PELEG,YINON SHLOMI,HAIM MOSKOWITZ,DEPHNA MIRON,AYELET		
		GILBOA,		
		PI MADELENE MIMON		
		PC		
		CLIN15/09,C07K16/40,C12N1/19,C12N1/21,C12N5/10,C12N9/24,C12N15/		
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		CC Topology: Linear;		
		CC Cells genetically modified for expressing recombinant		
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PF 14-MAY-2002
PR 29-APR-1999 JP 2000547200
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HANNA BEN ARTZI, WATTY AYAL, HERSHKOVITZ, ORON YACOB, ZEEVI, IRIS
PECKER,
PI YOAV PELEG, YINON SHLOMI, HAIM MOSKOWITZ, DEPHNA MIRON, AYELET
GILBOA,
PI MADELENE MIRON
PC
C12N15/09, C07K16/40, C12N1/19, C12N1/21, C12N5/10, C12N9/24, C12N15/ PC
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CC Topology: linear;
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heparanase and
CC method, and method of purifying recombinant heparanase. FH
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION	AR194189			linear
VERSION	AR194189.1			FAT 20-APR-2002
KEYWORDS	GI:20240781			
SOURCE	.			
ORGANISM	Unknown.			
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REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 1721)			
TITLE	Avai-Harschkovitz,M., Moskowitz,H., Miron,D., Gilboa,A., Mimoun,M., Ben-Artzi,H., Yacoby-Zeevi,O., Pecker,I., Peleg,Y. and Schloml,Y. Genetically modified cells and methods for expressing recombinant hepatenase and methods of purifying same Patent: US 6348344-A 1 19-FEB-2002;			
JOURNAL	Location/Qualifiers			
FEATURES	1..1721			
SOURCE				

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Matches 1721; Conservative	0.0;	Mismatches 0;		

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OY	481	TACGGTTGGAATGCGCCCTCACAGAGCAATTGCTACTCCAGAAACACTACCAAAAAAGT	540
Db	481	TACGGTTGGAATGCGCCCTCACAGAGCAATTGCTACTCCAGAAACACTACCAAAAAAGT	540
OY	541	TCAAGAACACACCTTACTCAAGAAGCTGTATATGTGCTATACCTTTTGCAAACTGCT	600
Db	541	TCAAGAACACACCTTACTCAAGAAGCTGTATATGTGCTATACCTTTTGCAAACTGCT	600
OY	601	CAGACCTGGACTTGATCTTTGSCCTTAATGCGTTATTAAAGACAGCAGATTTGCAGTGA	660
Db	601	CAGACCTGGACTTGATCTTTGSCCTTAATGCGTTATTAAAGACAGCAGATTTGCAGTGA	660
OY	661	ACAGTTCTAATGCTCAGTGTCTCTGGACTACGCTCTTCCAAAGGGATTAACATTCTT	720

Db	661	ACGHTCTAATCTCAGTGGCTCCCGAGCTACTGCTCTCCAAAGGGGTATACATTCTT	1720
Qy	721	GGGAATCAGGCATGACCTAAACGTTCTCTTAAGAAAGCGATATTTCATCAATGGGT	780
Db	721	GGGAATCAGGCATGACCTAAACGTTCTCTTAAGAAAGCGATATTTCATCAATGGGT	780
Qy	781	CGAGTTGAGGAATAATTAATTCAATTGCAATTAACCTTCTAAGAAAGTCACCTTCAAA	840
Db	781	CGAGTTGAGGAATAATTAATTCAATTGCAATTAACCTTCTAAGAAAGTCACCTTCAAA	840
Qy	841	ATGCAAAACCTATAGTCTGATGTTGGTACGCTCGAAGAAAGCGCTAAGATGCTGA	900
Db	841	ATGCAAAACCTATAGTCTGATGTTGGTACGCTCGAAGAAAGCGCTAAGATGCTGA	900
Qy	901	AGAGCTCTCTAAGGCTGGTGGAGAAAGTGAATGATTCAATTCATAGTCATCACTAAT	960
Db	901	AGAGCTCTCTAAGGCTGGTGGAGAAAGTGAATGATTCAATTCATAGTCATCACTAAT	960
Qy	961	TGAATGACCGGACTGCTACCGAGGAGATTTTCTAAACCTGATGATATGGAACATTTT	1020
Db	961	TGAATGACCGGACTGCTACCGAGGAGATTTTCTAAACCTGATGATATGGAACATTTT	1020
Qy	1021	TTTCATCTGTCGCAAAAAGTTTCCAGTGTGTTGAGAGCCAGGCTGCGAAGAAAGTCT	1080
Db	1021	TTTCATCTGTCGCAAAAAGTTTCCAGTGTGTTGAGAGCCAGGCTGCGAAGAAAGTCT	1080
Qy	1081	GCTTAGAGAAACAAGCTGTGCATATGAGAGCGCGCTTGTCTATCCGACCTTTG	1140
Db	1081	GCTTAGAGAAACAAGCTGTGCATATGAGAGCGCGCTTGTCTATCCGACCTTTG	1140
Qy	1141	CAGCTGCTTTATGTGGCTGAGATAAATTGGGCTGTCCAGCCCGAATGGGAATAGAGTG	1200
Db	1141	CAGCTGCTTTATGTGGCTGAGATAAATTGGGCTGTCCAGCCCGAATGGGAATAGAGTG	1200
Qy	1201	TGATGAGGCAAGATTTCTTTGAGAGCAAGAACTACATTATAGTGATGAATCTTCATC	1260
Db	1201	TGATGAGGCAAGATTTCTTTGAGAGCAAGAACTACATTATAGTGATGAATCTTCATC	1260
Qy	1261	CTTTACCTGATTAATTGGCTATCTCTTCTGTCAAGAAATGGTGGGACCAAGGTGTA	1320
Db	1261	CTTTACCTGATTAATTGGCTATCTCTTCTGTCAAGAAATGGTGGGACCAAGGTGTA	1320
Qy	1321	TGGCAAGCGTGCAGGTTCCAAAGAGAAAGCTTCGATTAACCTTCATTTGACAAACA	1380
Db	1321	TGGCAAGCGTGCAGGTTCCAAAGAGAAAGCTTCGATTAACCTTCATTTGACAAACA	1380
Qy	1381	CTGACATCCAAAGTATTAAGAAGGAGATTAACTCTGTATGCGATTAACCTTCATAG	1440
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Qy	1561	TAAAGATGATGATGATCAAACTGTGCACTTTAATGAAAAACTCTCGGCGCAGGAA	1620
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RESULT 10

AR194190 1721 bp DNA linear PAT 20-APR-2002
LOCUS AR194190
DEFINITION Sequence 3 from patent US 6348344.
ACCESSION AR194190
VERSION AR194190.1 GI:20240782
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1721)
AUTHORS Ayal-Hershkovitz,M., Moskowitz,H., Miron,D., Gilboa,A., Mimon,M.,
Ben-Artzi,H., Yacoby-Zeevi,O., Pecker,I., Peleg,Y. and Schiomi,Y.
TITLE Genetically modified cells and methods for expressing recombinant
heparanase and methods of purifying same
JOURNAL Patent: US 6348344-A 3 19-FEB-2002;
FEATURES
Location/Qualifiers
1..1721
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 1721; DB 6; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 11
AR221285 1721 bp DNA linear PAT 26-SEP-2002
LOCUS AR221285
DEFINITION Sequence 1 from patent US 6426209.

ACCESSION AR221285
VERSION AR221285.1 GI:23328256
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1721) Pecker, I. and Yacoby-Zeevi, O.
AUTHORS Ayal-Herskovitz, M.,
TITLE Genetically modified cells and methods for expressing recombinant
heparanase and methods of purifying same
JOURNAL Patent: US 6426209-A 1 30-JUL-2002;
FEATURES Location/Qualifiers
source 1. 1721
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ORIGIN

Query Match 100.0%; Score 1721; DB 6; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CTAAAGCTTTGACTCTCCGCTGCGCGCAAGCTGGCGGGGAGACGCGCAAGGAGCCCA 60
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RESULT 12
AR221286
LOCUS AR221286 1721 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 3 from patent US 6426209.
ACCESSION AR221286
VERSION AR221286.1 GI:23328257
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1721)
AUTHORS Ayal-HersHKovltz,M., Pecker,I. and Vachoby-Zeevi,O.
TITLE Genetically modified cells and methods for expressing recombinant
heparanase and methods of purifying same
JOURNAL Patent: US 6426209-A 3 30-JUL-2002;
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 1721; DB 6; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
AR243203
LOCUS AR243203 1721 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6475763.
ACCESSION AR243203
VERSION AR243203.1 GI:27290318
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1721)
AUTHORS Ayal-HersHKovltz,M., Moskowltz,H., Miron,D., Gilboa,A., Mimon,M.,

JOURNAL Patent: US 6475763-A 3 05-NOV-2002;
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ORGANISM Unknown.
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AUTHORS Pecker,I., Vlodavsky,I., Friedman,Y. and Peretz,T.
TITLE Heparanase specific molecular probes and their use in research and medical applications
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GenCore version 5.1.6
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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HTC; CNSLUT_CDNA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@lifetech.com URL: <http://fulllength.invitrogen.com/InvitrogenCorporation1600>
Faraday Avenue
2 (bases 1 to 1685)
REFERENCE
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage :
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqlife@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
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into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
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RESULT 2
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 DEFINITION full-length cDNA clone CSOD1028Y04 of Placenta Cot 25-normalized
 ACCESSION CR610536
 VERSION CR610536.1 GI:50491343
 KEYWORDS HTC; cDNA; cDNA
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1665)
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 CONTACT Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
 REMARK 2 (bases 1 to 1665)
 REFERENCE Genoscope.
 AUTHORS Direct Submission
 TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
 FEATURES Location/Qualifiers
 1..1665 source


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/organism="Homo sapiens"
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ORIGIN

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Query Match      96.0%; Score 1651.6; DB 3; Length 1665;
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Matches 1654; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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DB 1568 TAAAGATGTTGATGATCAACCTTGGCACTTTAATGAGAAACCTTCCGGCCAGGAA 1627
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DB 1628 GTTCACTGGGCTTGCAGCTTTCATATTAATTTT 1665
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RESULT 3
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LOCUS
DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
library, clone:A430101M04 product:hepatanase, full insert sequence.
ACCESSION AK040471.1 GI:26333764
VERSION AK040471.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
AUTHORS High-efficiency full-length cDNA cloning
TITLE Mech. Enzymol. 303, 19-44 (1999)
JOURNLS 99279253
MEDLINE 10349636
PUBMED
REFERENCE
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
```

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
MEDLINE Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 20499374
REFERENCE 11042159
AUTHORS 3

TITLE Shihata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Komoto, H., Akiyama, J., Nishi, K., Kitanai, T., Tashiro, H., Itoh, M.,
Suzuki, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Murakami, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
Riken integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL 20530913
MEDLINE
PUBMED 11076861
REFERENCE
AUTHORS 4

TITLE The RIKEN Genome Exploration Research Group Phase II Team and the
JOURNAL FANTOM Consortium.
MEDLINE Functional annotation of a full-length mouse cDNA collection
PUBMED Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS

TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research
JOURNAL Group Phase I & II Team.
MEDLINE Analysis of the mouse transcriptome based on functional annotation
PUBMED Nature 420, 563-573 (2002)
REFERENCE 6
AUTHORS (bases 1 to 2173)

TITLE Aichi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, Y., Kojima, Y., Kondo, S., Komoto, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Murakami, M., and Hayashizaki, Y.
JOURNAL Direct Submision
MEDLINE Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of
PUBMED Physical and Chemical Research (RIKEN), Laboratory for Genome
REFERENCE Exploration and Chemical Research (RIKEN), Laboratory for Genome
AUTHORS RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

1. 2173

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ORIGIN

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Matches 1291; Conservative 0; Mismatches 329; Indels 0; Gaps 0;
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Contact: Genoscope - Centre National de Séquençage
2 rue Gaston Crémieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: sequ@genoscope.cns.fr, web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-*olligo*(dT) primer. Five primers
enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalised. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
2469.r
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?b=CS001059CG08ND1&c=2469.r>.

FEATURES

Source

1. .1035

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primer. Five primers and enriched, double-strand cDNA was
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sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN

Query Match

55.4%; Score 952.6; DB 1; Length 1035;

Matches 969; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

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Db 987 YTTCCAAGGCTAWTACATTTCTTGGRACCTAGGCAATGCACTACAG-TTCCTTAAGAA 929

58 GGCCTGATATTTTCATCATGCGTCGACATTAGGAGAGATTATATTCATTGCATAACT 817

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Db 748 AGTTACATGGCATCACTACTATTGAAATGGACGACTGCTACCAGGAGAGATTCTTCTAA 689

998 CCTGATGTA TTGACATTTTATTTCATCTGCGAAAGTTTCCAGGTGTGAGAG 1057

Db 688 CCCTGATGTA TTGACATTTTATTTTCATCTGTGCAAAAGTTTCCAGGTGTTGAGAG 629

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569

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[illegible]

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Db 448 TTAGTGGATGAAACTTCGATCCTTACCGATGATTAATGGCAATCTCTCTGTCAGAA 389

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LOCUS	AK087283	1962 bp	mRNA linear HTC 03-APR-2004
DEFINITION			Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched library, clone:EO30042C09 product:hepatanase, full insert sequence.
ACCESSION	AK087283		
VERSION	AK087283.1	GI:26104170	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasai, M., Fujiwaka, S., Inoue, K., Togawa, Y., Tanaka, M., Ohara, E., Watabiki, M., Yoneeda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system-384-Format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE			
AUTHORS	4		
TITLE	THE RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.		
JOURNAL	Functional annotation of a full-length mouse cDNA collection		
REFERENCE	Nature 409, 685-690 (2001)		
AUTHORS	5		
TITLE	THE PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		

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Qy 378 CCNAGAGAGATCAACCTTTGAGAGAGAGATTACCTGCAATCTCAAGTCAACCAAGAT 437
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Db 1428 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 1487
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Db 1488 GTACCGGCTCGTGTTCAGAGAAACAGTGTATGATCACTTGTGAAGCTTCGGGGCGG 1547
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RESULT 6
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LOCUS 1026 bp mRNA linear EST 30-MAR-2004
DEFINITION AL552174 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSOD1059YN15 5-PRIME, mRNA sequence.
ACCESSION AL552174
VERSION AL552174.3 GI:45856963
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1. (bases 1 to 1026)
L.I.W.B., Gruber, C., Jessee, J. and Polyes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT
On Feb 15, 2001 this sequence version replaced gi:31273990.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
2469.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna7s=CSOD1059CG08P1&c=2469.r.
FEATURES
location/Qualifiers
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/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 53.7%; Score 923.6; DB 1; Length 1026;
Best Local Similarity 98.4%; Pred. No. 6.2e-244;
Matches 956; Conservative 7; Mismatches 6; Indels 3; Gaps 3;
Qy 1 CTAGAGCTTTGAGCTTCCTCGGCGGAGCTGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 60
Db 1 CTAGAGCTTCGACTTTCCTGCGC-GCACTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 59
Qy 61 AGATGCTGCTGCGCTGAGAGCTGCGCGCGCGCTGATGCTGCTGCTGCGGAGCT 120
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Db 120 CGCTGGGTCCCTCTCCCTGCGCGCGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 179
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Qy 241 CCATGAGCGCAACCTGCGCAGAGCCGCGGTTCTCTATCTCTGCGGTTCTCCAAAGC 300

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Qy      781 CGCAGTTAGAGAGATTAATATTAATCAATTTGCTTAAGAAAGTCCACTTCAAAA 840
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RESULT 7
AL545270 945 bp mRNA linear EST 25-MAR-2004
LOCUS DEFINITION AL545270 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
ACCESSION AL545270
VERSION AL545270.3 GI:45745753
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 945)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:11267106.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

```

FEATURES
source
1..945
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS010281P04"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2469.r

For more information about this cluster, see <http://www.genoscope.cns.fr/cdna?ls=CS010281P04&c=2469.r>.

Query Match 52.4%; Score 902.6; DB 1; Length 945;
Best Local Similarity 99.3%; Pred. No. 3.9e-238;
Matches 916; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Qy      4 GAGCTTTCAGCTCTCCGCTGCGCGGAGCTGCGGGGAGAGCAGCCAGGTGAGCCCAAGA 63
Db      10 GGGATTCGACCTCTCCGCTGCGCGGAGCTGCGGGGAGAGCAGCCAGGTGAGCCCAAGA 69
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Db      70 TGCTGCTGCGCTGGAAGCTGCGCGCTGCGCGCGCGGTATGCTGCTGCTCTGGGCGCG 129
Qy      124 TGGTCCCTCTTCCCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 183
Db      130 TGGTCCCTCTTCCCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 189
Qy      184 TGGACTTTCACCCAGAGAGCGGCTGCACTGTGAGACCCCTGCTCTGCTCGTCACCA 243
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Qy      244 TTGACGCAACCTGCGCAAGCAGACCGCGGTCTCATCTCTCTGGGTTCTCCAAAGCTTC 303
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Qy      484 GGTGGAATGCGCTTACCAAGAGCAATGCTACTCTCCAGAACTACCAAGAAAGTTCA 543
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Qy      664 GTTCTAATGCTCAGTTGCTCTGAGACTACTGCTTCCAGAGGGGTATTAACATTTCTTGGG 723
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QY	724	AACTAGGCAATGAACCTTAAAGTTTCCCTTAAGAACGCTGATATTTTCATCAATGGGTGGC		783
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QY	784	AGTTAGGAGGAAGATTATATTCATTCATTCATTAACCTTCTAAGAAAGTCCACTTCAAAAATG		843
Db	790	AGTTAGGAGGAAGATTATATTCATTCATTCATTAACCTTCTAAGAAAGTCCACTTCAAAAATG		849
QY	844	CAAAACTCTAATGCTCTGATGTGGTCAAGCTTCGAAGAAAGACGGCTTAAGATGCTGAAGA		903
Db	850	CAAAACTCTAATGCTCTGATGTGGTCAAGCTTCGAAGAAAGACGGCTTAAGATGCTGAAGA		909
QY	904	GCTTCCTGAGGCTGCTGGAGA	925	
Db	910	GCTT-CTGAAGGCTGTGTGAGA	930	
RESULT 8				
LOCUS	AL545232/c			
DEFINITION	AL545232	1027 bp	mRNA	linear
ACCESSION	AL545232	1027 bp	mRNA	linear
VERSION	AL545232.3	GI:45745716		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1. (bases 1 to 1027)			
JOURNAL	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.			
COMMENT	Full-length cDNA libraries and normalization			
	unpublished (2001)			
	On Feb 15, 2001 this sequence version replaced gi:31267068.			

Genoscope - Centre National de Séquençage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: beta@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five primers
end enriched, double-stranded cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by life technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
2469.r

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?n=CS0D1028BC02NP1KC-2469.r>.

FEATURES	Location/Qualifiers
source	1. .1027

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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CS0D10281F04"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dr)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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[illegible]

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Qy	1005	GTATTTGGACATTTTATTTTCACTCTGTGCAAAAAGTTTCCAGGTGTGTGAGACACCAAG	1066
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Qy	1125	CTATCCGACACCTTTGGAGCTGTGCTTTATGTGCTGTGATAAATTGGGCTGTACCCGA	1184
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Qy	1185	ATGGGAATAGAAAGTGTGTGATGAGGCAAGATATCTTTGGAGCAGAAACTACCATTTAGTG	1244
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Qy	1245	GATGAAAACCTTGCATCCTTTACTCTGATTTATGGCTATCTCTTCTGTTCAAGAAATTGGTG	1304
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Qy	1485	GTGATTAATAATCCTTTCTPAAGACTTTTGGGACCTCATGATTTACTTTCCAAATCTGTCCAA	1544
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Qy	1545	CTCAATGTCATACTCTPAAGAATGTGGATGATCAAACTTGGCAACCTTATATGGAATAA	1604
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Qy	1605	CCTCTCCGGCAGGAAGTTCACTGGGCTTGGCAGCTTTCATATAGTTTATTTT 1658	
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RESULT 9			
LOCUS	BX398409/c		
DEFINITION	BX398409 Homo sapiens PLACENTA 1066 bp cDNA	linear	EST 29-APR-2004
ACCESSION	BX398409		
VERSION	clone CSDDI058Y124.3-PRIME, mRNA sequence.		
KEYWORDS	BX398409, BX398409.2	GI:46873668	
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 1066)		
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Poyaves, D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	On May 13, 2003 this sequence version replaced gi:30617572.		
	Contact: Genoscope		
	Genoscope - Centre National de Sequencage		
	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE		
	Email: seiref@genoscope.cns.fr, Web : www.genoscope.cns.fr		


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Db      480  CTCAAGTACACAGATATTTTGCATTAATGATCCATCCCTCTGATGTAGAGAGAGT 539
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DEFINITION AGNCOURT_8343629 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6250265
VERSION    BO691142
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
  AUTHORS  Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
  TITLE    NIH-MGC http://mgi.nci.nih.gov/.
  JOURNAL  National Institutes of Health, Mammalian Gene Collection (MGC)
  COMMENT  Unpublished (1999)
           Contact: Robert Strusberg, Ph.D.
           Email: cga@db-remail.nih.gov
           Tissue Procurement: ATCC
           cDNA Library Preparation: Rubin Laboratory
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LINL at:
           http://image.lnl.gov
           Plate: L10CM2393 row: a column: 18
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               /clone_1b="NIH_MGC_110"
               /note="Organ: pancreas; Vector: pOTB7; Site: 1; XhoI;
               Site: 2; EcoRI; cDNA made by oligo-dT priming.
               Directionally cloned into EcoRI/XhoI sites using the
               following 5' adaptor: GGCACGAG(G). Library constructed by
               Ling Hong in the laboratory of Gerald M. Rubin (University
               of California, Berkeley) using ZAP-cDNA synthesis kit
               (Stratagene) and Superscript II RT (Life Technologies).
               Note: this is a NIH_MGC Library."

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ORIGIN

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Query Match      43.6%; Score 750.2; DB 5; Length 924;
Best Local Similarity 95.4%; Pred. No. 6.2e-196;
Matches 781; Conservative 0; Mismatches 37; Indels 1; Gaps 1;

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Qy      152  CCGAGCTGCGGAAGACAGAGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 211
Db      224  CCGAGCTGCGGAAGACAGAGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 283
Qy      212  CTTGTTGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 271
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Db      344  GTTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 403
Qy      332  GTAACCTGAGGTTTGTGGGACCAAGACAGACTTCTTAATTTTTCATCCCAAGAGGATC 391
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Qy      392  AACCTTGAAGAGAGAGAGGTTATCTGCAATCTCAAGTCAACAGATATTTTGGCAATATG 451
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Qy      452  ATCCATCCCTGCTGATGTCGAGAGAGAGGTTAGGTTGAGAGGCTTCCACAGAGCAAT 511
Db      524  ATCCATCCCTGCTGATGTCGAGAGAGGTTAGGTTGAGAGGCTTCCACAGAGCAAT 583
Qy      512  GCTATCCGAGAACACATCAAGAGAGAGGTTCAAGAGAGCACTTCAAGAGGCTGCTG 571
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RESULT 13
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LOCUS      BO438834
DEFINITION AGNCOURT_7761619 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6017952
VERSION    BO438834
KEYWORDS   5', mRNA sequence.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Oy 1556 AACTCTAAGAATGGTGGATGATCAAA-CCTTGCCACCTTTAATGAAAAA-CCTCTCCGG 1613
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Db 547 AACTCTAAGAATGGTGGATGATCAAAACCCTTGCCACCTTTAATGAAAAAACCCTCTCCGG 606
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Oy 1614 CCAGGAATTCACCTGGGCTTGCCAGCTTTCATATAGTTTTTTG 1659
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 23:07:32 ; Search time 890 Seconds
(without alignments)
11447.050 Million cell updates/sec

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Perfect score: 1721
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1721	100.0	1721	2	AAX35648
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23	1686.8	98.0	3726	2	AAX86671	Aax86671 CDNA enco
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25	1686.8	98.0	3726	12	ADK51968	Adk51968 Human ato
26	1686.8	98.0	3726	12	ADN04901	Adn04901 Antipapori
27	1686.8	98.0	3726	13	ADN05073	Adn05073 Antipapori
28	1686.8	98.0	3726	13	ADN080253	Adn080253 Hepatoma
29	1686.8	98.0	3726	14	ADP25078	Adp25078 PRO poly
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31	1648	95.8	1673	12	AD063816	Ad063816 Human hep
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33	1646.4	95.7	1673	12	AD063818	Ad063818 Human hep
34	1631.4	94.8	1669	8	ABZ22816	Abz22816 Human hep
35	1631.4	94.8	1669	10	ADL16011	Adl16011 G-coupled
36	1629.8	94.7	1669	12	ADL39950	Adl39950 Human G-c
37	1585	92.1	1593	2	AAZ11236	Aaz11236 Human pre
38	1554.2	90.3	1625	12	AD063819	Ad063819 ChimERIC
39	1554.2	90.3	1625	12	AD063820	Ad063820 ChimERIC
40	1552.6	90.2	1625	12	AD063821	Ad063821 ChimERIC
41	1535	89.2	1584	6	ABL40753	Abi40753 Chicken s
42	1535	89.2	1584	10	AD63532	Ad63532 ChimERIC
43	1092	63.5	2396	3	AA75081	Aa75081 CDNA enco
44	1092	63.5	2396	4	AA91113	Aa91113 Mouse hep
45	1092	63.5	2396	10	ADG88833	Adg88833 Mouse hpa

ALIGNMENTS

RESULT 1

ID AAX35648 standard; CDNA; 1721 BP.

AC AAX35648;

DT 09-JUL-1999 (first entry)

DE CDNA encoding a human heparanase protein.

KW Heparanase; hpa; modulator; heparin-binding growth factor;
KW cellular response; cytokine; cell interaction; plasma lipoprotein;
KW cellular susceptibility; infection; disintegration;
KW neurodegenerative plaque; wound healing; angiogenesis;
KW atherosclerosis; inflammation; neurodegenerative disease; neuritis;
KW plasma heparin; micrometastasis; autoimmune lesion; renal failure; ss.

OS Homo sapiens.

PN W09911798-A1.

PD 11-MAR-1999.

PF 31-AUG-1998; 98WO-US017954.

PR 02-SEP-1997; 97US-00922170.

PR 02-JUL-1998; 98US-00109386.

PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.

PI Pecker I, Vlodavsky I, Feinstein E;

DR WPI; 1999-302255/25.

DR P-PSDB; AAY02345.

PT New human polynucleotide useful for treating angiogenesis, restenosis,
PT and inflammation.

PS Claim 4; Fig 1; 63pp; English.

XX The specification describes a polypeptide having heparanase (hpa)

CC activity. The recombinant protein is used as a modulator of heparin-
 CC binding growth factors, cellular responses to heparin-binding growth
 CC factors and cytokines, cell interaction with plasma lipoproteins,
 CC cellular susceptibility to viral, protozoal and bacterial infections
 CC or disintegration of neurodegenerative plaques. Heparanase may be useful for
 CC conditions such as wound healing, angiogenesis, restenosis,
 CC atherosclerosis, inflammation, neurodegenerative diseases, and viral
 CC infections. Mammalian heparanase can be used to neutralize plasma
 CC heparin, and anti-heparanase antibodies may be applied for
 CC immunodetection and diagnosis of micrometastases, autoimmune lesions, and
 CC renal failure in biopsy specimens, plasma samples, and body fluids. The
 CC present sequence encodes human heparanase

SO Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match 100.0%; Score 1721; DB 2; Length 1721;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CTGAGAGCTTTCGACTCTCGCTGCGCGGCACTGCGCGGAGGAGAGCAGCAGGAGAGCCCA 60
DB 1 CTGAGAGCTTTCGACTCTCGCTGCGCGGCACTGCGCGGAGGAGAGCAGCAGGAGAGCCCA 60
QY 61 AGATGCTGCTGCGCTGGAAGCCCTGCGCTGCGCGGAGGAGAGCAGCAGGAGAGCCCA 120
DB 61 AGATGCTGCTGCGCTGGAAGCCCTGCGCTGCGCGGAGGAGAGCAGCAGGAGAGCCCA 120
QY 121 CGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 180
DB 121 CGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 180
QY 181 ACTGAGACTTTCGACTCTCGCTGCGCGGCACTGCGCGGAGGAGAGCAGCAGGAGAGCCCA 240
DB 181 ACTGAGACTTTCGACTCTCGCTGCGCGGCACTGCGCGGAGGAGAGCAGCAGGAGAGCCCA 240
QY 241 CCATTGAGCGCAACCTGCGCGGCACTGCGCGGAGGAGAGCAGCAGGAGAGCCCA 300
DB 241 CCATTGAGCGCAACCTGCGCGGCACTGCGCGGAGGAGAGCAGCAGGAGAGCCCA 300
QY 301 TTGCGAGCTTTCGACTCTCGCTGCGCGGCACTGCGCGGAGGAGAGCAGCAGGAGAGCCCA 360
DB 301 TTGCGAGCTTTCGACTCTCGCTGCGCGGCACTGCGCGGAGGAGAGCAGCAGGAGAGCCCA 360
QY 361 ACTTCTTAATTTTCGACTCTCGCTGCGCGGCACTGCGCGGAGGAGAGCAGCAGGAGAGCCCA 420
DB 361 ACTTCTTAATTTTCGACTCTCGCTGCGCGGCACTGCGCGGAGGAGAGCAGCAGGAGAGCCCA 420
QY 421 CTGAGAGCTTTCGACTCTCGCTGCGCGGCACTGCGCGGAGGAGAGCAGCAGGAGAGCCCA 480
DB 421 CTGAGAGCTTTCGACTCTCGCTGCGCGGCACTGCGCGGAGGAGAGCAGCAGGAGAGCCCA 480
QY 481 TACGAGTGAATGCGCTGCGCTGCGCGGCACTGCGCGGAGGAGAGCAGCAGGAGAGCCCA 540
DB 481 TACGAGTGAATGCGCTGCGCTGCGCGGCACTGCGCGGAGGAGAGCAGCAGGAGAGCCCA 540
QY 541 TCAGAGACAGCACTTCAAGAGCTCTGAGATGCTGCTGAGATGCTGAGATGCTGAGATGCTGAG 600
DB 541 TCAGAGACAGCACTTCAAGAGCTCTGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAG 600
QY 601 CAGAGAGCTGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAG 660
DB 601 CAGAGAGCTGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAG 660
QY 661 ACAAGTGAATGCTGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAGATGCT 720
DB 661 ACAAGTGAATGCTGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAGATGCT 720
QY 721 GGAAGACAGCACTTCAAGAGCTCTGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAG 780
DB 721 GGAAGACAGCACTTCAAGAGCTCTGAGATGCTGAGATGCTGAGATGCTGAGATGCTGAG 780
QY 781 CGCAGTGAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840
DB 781 CGCAGTGAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840

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DB 781 CGCAGTGAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840
QY 841 ATGCAAACTCTATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 841 ATGCAAACTCTATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 901 AGAGCTTCTGAGAGGCTGCTGAGAGGCTGCTGAGAGGCTGCTGAGAGGCTGCTGAGAGGCTG 960
DB 901 AGAGCTTCTGAGAGGCTGCTGAGAGGCTGCTGAGAGGCTGCTGAGAGGCTGCTGAGAGGCTG 960
QY 961 TGAATGAGAGGAGCTGCTGAGAGGCTGCTGAGAGGCTGCTGAGAGGCTGCTGAGAGGCTG 1020
DB 961 TGAATGAGAGGAGCTGCTGAGAGGCTGCTGAGAGGCTGCTGAGAGGCTGCTGAGAGGCTG 1020
QY 1021 TTTTATCTGTCGCAAAAAGTTTTCAGAGGCTGCTGAGAGGCTGCTGAGAGGCTGCTGAGAG 1080
DB 1021 TTTTATCTGTCGCAAAAAGTTTTCAGAGGCTGCTGAGAGGCTGCTGAGAGGCTGCTGAGAG 1080
QY 1081 GGTGAGAGAGAGAGCTGCTGAGAGGCTGCTGAGAGGCTGCTGAGAGGCTGCTGAGAGGCTG 1140
DB 1081 GGTGAGAGAGAGAGCTGCTGAGAGGCTGCTGAGAGGCTGCTGAGAGGCTGCTGAGAGGCTG 1140
QY 1141 CAGCTGCTTATGCTGCTGAGATTAATTTGGGCTGCTGAGAGGCTGCTGAGAGGCTGCTGAGAG 1200
DB 1141 CAGCTGCTTATGCTGCTGAGATTAATTTGGGCTGCTGAGAGGCTGCTGAGAGGCTGCTGAGAG 1200
QY 1201 TGATGAGAGAGAGATTTCTTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
DB 1201 TGATGAGAGAGAGATTTCTTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1261 CTTTACCTGATTAATTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
DB 1261 CTTTACCTGATTAATTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
QY 1321 TGGCAAGCTGCAAGGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 TGGCAAGCTGCAAGGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CTGAGATCAAGAGATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1381 CTGAGATCAAGAGATTAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 TCACCAAGATCTGCGGTTACCTTCTTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1441 TCACCAAGATCTGCGGTTACCTTCTTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1501 TAAAGACCTTGGAGAGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
DB 1501 TAAAGACCTTGGAGAGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
QY 1561 TAAAGATGCTGATGATCAAACTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
DB 1561 TAAAGATGCTGATGATCAAACTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 GTTCACTGGGCTTGGAGAGCTTCTGATTAATTAATTAATTAATTAATTAATTAATTAAT 1680
DB 1621 GTTCACTGGGCTTGGAGAGCTTCTGATTAATTAATTAATTAATTAATTAATTAATTAAT 1680
QY 1681 CTGCTTGCATCTGAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1721
DB 1681 CTGCTTGCATCTGAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1721

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RESULT 2
 AA239195
 ID AA239195 standard; cDNA; 1721 BP.
 XX AA239195;
 AC AA239195;
 XX 02-MAR-2000 (first entry)
 DT Human heparanase encoding cDNA.
 XX

KW Human; heparanase; hpa; genetic modification; expression; anticancer;
KW angiogenesis; anti-angiogenic; antiproliferative; antiviral; antitumor;
KW anti-atherosclerotic; anti-inflammatory; antineurodegeneration;
KW heparan sulphate; heparin-binding growth factor; tumor angiogenesis;
KW metastasis; wound healing; restenosis; atherosclerosis; inflammation;
KW neurodegeneration; viral infection; cystic fibrosis; cancer; diagnosis;
KW microvasculature; autoimmune lesion; kidney failure; ss.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 63..1694
FT /*tag= a
FT /product= "heparanase"
XX
XX MO9957244-A1.
XX
XX 11-NOV-1999.
XX
XX 29-APR-1999; 99WO-US009256.
XX
XX 01-MAY-1998; 98US-00071618.
XX 02-MAR-1999; 99US-00260038.
XX
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX (FRIE/) FRIEDMAN M M.
XX
XX Ben-Arzi H, Ayal-Hershkovitz M, Yacoby-Zeevi O, Pecker I;
XX Peleg Y, Shlomi Y;
XX
XX WPI; 2000-062144/05.
XX P-Psdb; AAY57590.
XX
XX Engineered cells that express recombinant heparanase, useful
XX therapeutically, e.g. for treating angiogenesis and to screen for
XX specific inhibitors, potential anticancer agents.
XX
XX Claim 2; Page 106-107; 118pp; English.
XX
XX The present invention describes genetically modified cells (A) containing
XX a polynucleotide (I) that encodes a polypeptide with heparanase activity,
XX and express recombinant heparanase (II). Heparanase cleaves heparan
XX sulphate (HS) at specific intrachain sites, resulting in release of
XX heparin-binding growth factors, enzymes and proteins that are sequestered
XX by HS in basement membranes, extracellular matrix or cell surfaces. It
XX may also be implicated in tumour angiogenesis and metastases. (II) is
XX potentially useful in wound healing and for treating angiogenesis;
XX restenosis, atherosclerosis, inflammation, neurodegeneration, viral
XX infection and cystic fibrosis. It can also be used to neutralise heparin
XX (an alternative to protamine) and to screen for specific inhibitors
XX (potentially useful for treating cancer and metastases). Antibodies
XX raised against (II) are used for immunodetection and diagnosis of
XX microvasculature, autoimmune lesions and kidney failure. (A) provide (II)
XX in large quantities, in a form that is homogeneously processed and
XX activated/neutralised by a dedicated protease. The present sequence
XX encodes human heparanase
XX
XX Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1721; DB 3; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTNAGACTTTCGACTCTCCGCTGCGCGGAGCTGCGGGGGAGACAGGAGTGAAGCCA 60
DB 1 CTNAGAGCTTTTCACCTCTCGCTGCGCGGAGCTGCGGGGGAGAGCAGCCAGGTGAGCCCA 60
QY 61 AGATGCTGCTGCGCTGAGAGCCTGCGCTGCGCGCGCGCTGAGTGCAGTCTCTCGAGGAC 120
DB 61 AGATGCTGCTGCGCTGAGAGCCTGCGCTGCGCGCGCGCTGAGTGCAGTCTCTCGAGGAC 120
QY 121 CGCTGGGCTCCCTCTCCCTGCGCGCTGCGCGCGCTGCGAGCCTGCGAGCAGAGCAGTCTG 180
DB 121 CGCTGGGCTCCCTCTCCCTGCGCGCTGCGCGCGCTGCGAGCCTGCGAGCAGAGCAGTCTG 180

DB 121 CGCTGGGCTCCCTCTCCCTGCGCGCTGCGCGCGCTGCGAGCCTGCGAGCAGAGCAGTCTG 180
QY 181 ACTGGAATCTTTCACCCAGAGAGCGGTGACCTGAGTGAAGCCCTGTTCTGTCCTGCA 240
DB 181 ACTGGAATCTTTCACCCAGAGAGCGGTGACCTGAGTGAAGCCCTGTTCTGTCCTGCA 240
QY 241 CCATTGAGCCCACTGCGCAGAGACCCGCGGTCTCTATCTCTCTGAGGTTCTCCAAAGC 300
DB 241 CCATTGAGCCCACTGCGCAGAGACCCGCGGTCTCTATCTCTCTGAGGTTCTCCAAAGC 300
QY 301 TTGCTGACTTGGCCAGAGAGGCTTGTCTCTGCTGATCTGAGTTGTGTGACCAAGACG 360
DB 301 TTGCTGACTTGGCCAGAGAGGCTTGTCTCTGCTGATCTGAGTTGTGTGACCAAGACG 360
QY 361 ACTTCTTAATTTTGGATCCCAAGAGGAATCACTTTGAAGAGAGATTACTGGCAAT 420
DB 361 ACTTCTTAATTTTGGATCCCAAGAGGAATCACTTTGAAGAGAGATTACTGGCAAT 420
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DB 421 CTCAAGTCACAGAGATATTTGCAAAATATGATCCATCTCTGATGTGAGAGAGAGT 480
QY 481 TACGTTGGAATGCGCTTACAGAGAGCAATTTCTACCTCCAGAGACATCAAGAAAAAGT 540
DB 481 TACGTTGGAATGCGCTTACAGAGAGCAATTTCTACCTCCAGAGACATCAAGAAAAAGT 540
QY 541 TCAAGAACAGACCACTACAGAGAGCTCTGATGATGCTATCACTTTTGAACCTGCT 600
DB 541 TCAAGAACAGACCACTACAGAGAGCTCTGATGATGCTATCACTTTTGAACCTGCT 600
QY 601 CAGAGCTGAGCTGATCTTTGCGCTTAAATGCGTTATTAAGAACAGCAGATTTTGACGTGA 660
DB 601 CAGAGCTGAGCTGATCTTTGCGCTTAAATGCGTTATTAAGAACAGCAGATTTTGACGTGA 660
QY 661 ACAGTTCTTAATGCTGATGCTCTGAGCTACTGCTCTTCAAGAGGATTAATTTCTT 720
DB 661 ACAGTTCTTAATGCTGATGCTCTGAGCTACTGCTCTTCAAGAGGATTAATTTCTT 720
QY 721 GGGAACTAGGCAATGAACCTTAACAGTTCTTAAAGAGGCTGATTTTCAATGAGGT 780
DB 721 GGGAACTAGGCAATGAACCTTAACAGTTCTTAAAGAGGCTGATTTTCAATGAGGT 780
QY 781 CGCAGTTAGAGAGATTAATTAATTCATTAATTAATTAATTAATTAATTAATTAATTA 840
DB 781 CGCAGTTAGAGAGATTAATTAATTCATTAATTAATTAATTAATTAATTAATTAATTA 840
QY 841 ATGCAAACTCTATGCTCTGATGTTGCTGAGCTCGAAGAAAGCGCTTAAGATGCTGA 900
DB 841 ATGCAAACTCTATGCTCTGATGTTGCTGAGCTCGAAGAAAGCGCTTAAGATGCTGA 900
QY 901 AGAGCTTCTGAGGCTGAGGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 960
DB 901 AGAGCTTCTGAGGCTGAGGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 960
QY 961 TGAATGAGCAGACTGCTACAGAGAGATTTTCTAAACCTGATGATTAATTAATTAATTA 1020
DB 961 TGAATGAGCAGACTGCTACAGAGAGATTTTCTAAACCTGATGATTAATTAATTAATTA 1020
QY 1021 TTTTATCTGTGCAAAAATTTTCCAGGTGTTGAGAGACCAAGGCTTGGCAAGAGTCT 1080
DB 1021 TTTTATCTGTGCAAAAATTTTCCAGGTGTTGAGAGACCAAGGCTTGGCAAGAGTCT 1080
QY 1081 GGTTAAGAGAAACAGCTCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1140
DB 1081 GGTTAAGAGAAACAGCTCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1140
QY 1141 CAGCTGCTTTATGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1200
DB 1141 CAGCTGCTTTATGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1200
QY 1201 TGATGAGCAAGATATTTTGTGAGAGCAAACTACATTTATGATGATGAATTAATTAATTA 1260
DB 1201 TGATGAGCAAGATATTTTGTGAGAGCAAACTACATTTATGATGATGAATTAATTAATTA 1260

QY	1261	CTTTACCTGATTTATTTGGCTATCTCTTGTTCAGAAAATGGTGGGCAACAAGTGTTAA	1320
Db	1261	CTTTACCTGATTTATTTGGCTATCTCTTGTTCAGAAAATGGTGGGCAACAAGTGTTAA	1320
QY	1321	TGGCAAGCGTGCAGAGGTTCAAAAGAGAAGGAACCTCGAGTAACTTATTTGCACAAACA	1380
Db	1321	TGGCAAGCGTGCAGAGGTTCAAAAGAGAAGGAACCTCGAGTAACTTATTTGCACAAACA	1380
QY	1381	CTGACATATCCAAAGGTATTAAGAAGAGATTTAACTCTGTATGCCATAAACCTCATACG	1440
Db	1381	CTGACATATCCAAAGGTATTAAGAAGAGATTTAACTCTGTATGCCATAAACCTCATACG	1440
QY	1441	TCACCAAGTACTTGGGGTTACCCATTCCTTTTCTAAACCAAGTGAATAAACTCTC	1500
Db	1441	TCACCAAGTACTTGGGGTTACCCATTCCTTTTCTAAACCAAGTGAATAAACTCTC	1500
QY	1501	TAAAGACCTTTGGGACCTCATAGATTACTTTCCAATCTGTCCAACTCAATGGTCTAACTC	1560
Db	1501	TAAAGACCTTTGGGACCTCATAGATTACTTTCCAATCTGTCCAACTCAATGGTCTAACTC	1560
QY	1561	TAAAGATGATGATATCATCAACCTTTTGAAGAAAAACCTCTCCGGCCAGGAA	1620
Db	1561	TAAAGATGATGATATCATCAACCTTTTGAAGAAAAACCTCTCCGGCCAGGAA	1620
QY	1621	GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGGATTAAGAAATGCCAAAGTTG	1680
Db	1621	GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGGATTAAGAAATGCCAAAGTTG	1680
QY	1681	CTGCTTGATCGAAAAATTAATAATTAATCTAGTCCGACACAG	1721
Db	1681	CTGCTTGATCGAAAAATTAATAATTAATCTAGTCCGACACAG	1721

RESULT 3	
AA75051	
ID	AAA75051 standard; cDNA; 1721 BP.
XX	
AC	AAA75051;
XX	
DT	15-JAN-2001 (first entry)
XX	
DE	cDNA encoding a human heparanase polypeptide.
XX	
KW	Human; heparanase; gene therapy; tumour; inflammation; autoimmunity; heparin-binding growth factor; cytokine; neurodegenerative plaque; wound healing; infection; burn; angiogenesis; restenosis; atherosclerosis; inflammation; neurodegenerative disease; Geissmann-Straussler Syndrome; Creutzfeldt-Jakob disease; ds.
XX	
OS	Homo sapiens.
Key	
FT	Location/Qualifiers
CDS	63..1693
FT	/tag= a
FT	/product= "heparanase"
stem_loop	698..724
FT	/tag= b
FT	/note= "these nucleotides are likely to be involved in forming stem and loop structures"
XX	
PN	WO200052178-A1.
XX	
PD	08-SEP-2000.
XX	
PF	14-FEB-2000; 2000WO-US003542.
XX	
PR	01-MAR-1999; 99US-00258892.
XX	
(INST-)	INSIGHT STRATEGY & MARKETING LTD.
(HADA-)	HADASIT MEDICAL RES SERVICES & DEV.
(FRIE/)	FRIEDMAN M M.
XX	

FI Peckert I, Vlodaavsky I, Feinstein E;
 XX WPI, 2000-579289/54.
 DR P-PSDB; AAB08849.
 XX
 XX New polynucleotides encoding a polypeptide having heparanase activity,
 PT useful in wound healing and in gene therapy, particularly in treating
 PT tumor, inflammation, autoimmunity, neurodegenerative diseases.
 PS
 PS Claim 9, Fig 1, 152pp; English.
 XX
 XX The present sequence encodes a human protein with heparanase catalytic
 CC activity. The heparanase (hpa) polynucleotide is useful in gene therapy,
 CC particularly in treating tumour, inflammation or autoimmunity.
 CC Particularly, the polynucleotide is useful in modulating the
 CC bioavailability of heparin-binding growth factors, cellular responses to
 CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
 CC interleukin (II)-8), cell interaction with plasma lipoproteins, cellular
 CC susceptibility to certain viral and some bacterial and protozoa
 CC infections, or disintegration of neurodegenerative plaques. The
 CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or
 CC radiation burns), and in the treatment of angiogenesis, restenosis,
 CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
 CC Strausler Syndrome or Creutzfeldt-Jakob disease), and some viral,
 CC bacterial or protozoa infections
 XX
 SO Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match	100.0%	Score 1721	DB 3	Length 1721	
Best Local Similarity	100.0%	Pred. No. 0			
Matches 1721	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	1	CTAGAGCTTTGCACTCTCCGCTGGCGCGGCACTGGCGGGGAGACAGCAAGTGAAGCCA	60		
Db	1	CTAGAGCTTTGCACTCTCCGCTGGCGCGGCACTGGCGGGGAGACAGCAAGTGAAGCCA	60		
QY	61	AGATGCTGCTGGCTCCGAAGCTTGCGTGGCCGCGCTGATGCTGCTGCTGGGGC	120		
Db	61	AGATGCTGCTGGCTCCGAAGCTTGCGTGGCCGCGCTGATGCTGCTGCTGGGGC	120		
QY	121	CGCTGGGCTCCCTCTCCCTGGCGCCGCGCGGACCTGGGCAAGCAACAGACCTGCTGG	180		
Db	121	CGCTGGGCTCCCTCTCCCTGGCGCCCTGCGCGGACCTGGGCAAGCAACAGACCTGCTGG	180		
QY	181	ACCTGACATTCTTACCCGAGAGCGCGTGCACCTGTGAAGCCCTCGTTCCTGTCGCTCA	240		
Db	181	ACCTGACATTCTTACCCGAGAGCGCGTGCACCTGTGAAGCCCTCGTTCCTGTCGCTCA	240		
QY	241	CCATTGACGCGCAACCTGAGCAGAGACCGGGGTTCCATGCTCTCTGGGTTCTCCAAAGC	300		
Db	241	CCATTGACGCGCAACCTGAGCAGAGACCGGGGTTCTCATCTCTGGGTTCTCCAAAGC	300		
QY	301	TTGCTACCTTGGCCAGAGGCTTGTCCTGCGTACCTGAGGTTGGTGAGCACCAGACAG	360		
Db	301	TTGCTACCTTGGCCAGAGGCTTGTCCTGCGTACCTGAGGTTGGTGAGCACCAGACAG	360		
QY	361	ACTTTCCTAATTTTCGATCCCAAGAAAGATCAACTTTGAAGAAGAAATTACTGCAAT	420		
Db	361	ACTTTCCTAATTTTCGATCCCAAGAAAGATCAACTTTGAAGAAGAAATTACTGCAAT	420		
QY	421	CTCAAGTCAACAGGATATTTGCAATATGATATTCATCCCTCGTAAATGGAGAGAAAGT	480		
Db	421	CTCAAGTCAACAGGATATTTGCAATATGATATTCATCCCTCGTAAATGGAGAGAAAGT	480		
QY	481	TACGTTTGAATGAGCCCTTACAGAGACAAATTGCTACTCCGAGAACTCAACGAAAAAGT	540		
Db	481	TACGTTTGAATGAGCCCTTACAGAGACAAATTGCTACTCCGAGAACTCAACGAAAAAGT	540		
QY	541	TCAGAGAACGACACTTACTCAAGAGGCTGTGATATGTGTATATCACTTTTGCAACTGCT	600		
Db	541	TCAGAGAACGACACTTACTCAAGAGGCTGTGATATGTGTATATCACTTTTGCAACTGCT	600		
QY	601	CAGGACTGCACTTATCTTTGGCCTTAATAGCGTTTATAGAACACACAGATTTGCAGTGA	660		

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Db      ||| 601 CAGAGCTGACTGATCTTTGGCTAAATGCGTATATTAAGAACACAGATTGGACGTGA 660
Qy      ||| 661 ACAGTTCTAAAGCTCAGTTGCTCTCGACTACTGCTCTTCCCAAGGGATTAACATTTCTT 720
Db      ||| 661 ACAGTTCTAAAGCTCAGTTGCTCTCGACTACTGCTCTTCCCAAGGGATTAACATTTCTT 720
Qy      ||| 721 GGGAACTAGGCAATGAACTTAACAGTTTCTTAAAGAGGCTGATATTTTCATCAATGGGT 780
Db      ||| 721 GGGAACTAGGCAATGAACTTAACAGTTTCTTAAAGAGGCTGATATTTTCATCAATGGGT 780
Qy      ||| 781 CGCAGTTAGGAGAGATTAATATTCATTAATGATTAACCTTCTAAGAAAGTCCACTTCAAAA 840
Db      ||| 781 CGCAGTTAGGAGAGATTAATATTCATTAATGATTAACCTTCTAAGAAAGTCCACTTCAAAA 840
Qy      ||| 841 ATGCAAACTCTATAGTCTCTGATGTTGGTCAAGCCCTCGAAGAAAGACGGCTAAGATGCTGA 900
Db      ||| 841 ATGCAAACTCTATAGTCTCTGATGTTGGTCAAGCCCTCGAAGAAAGACGGCTAAGATGCTGA 900
Qy      ||| 901 AGAGCTTCTGAAAGGCTGGTGGAGAAAGTATGATTAATGATTAATGATTAATGATTAATG 960
Db      ||| 901 AGAGCTTCTGAAAGGCTGGTGGAGAAAGTATGATTAATGATTAATGATTAATGATTAATG 960
Qy      ||| 961 TGAATGACGGAAGCTGCTACCAAGGAAAGATTTTCTAAACCTGATGATTTGAACATTTTGA 1020
Db      ||| 961 TGAATGACGGAAGCTGCTACCAAGGAAAGATTTTCTAAACCTGATGATTTGAACATTTTGA 1020
Qy      ||| 1021 TTTCAATCTGTGCAAAAAGTTTCCAGGCTGTGTAAGACACCGGCTGGCAAGAAAGTCT 1080
Db      ||| 1021 TTTCAATCTGTGCAAAAAGTTTCCAGGCTGTGTAAGACACCGGCTGGCAAGAAAGTCT 1080
Qy      ||| 1081 GATTAGGAGAAACAAGCTCTGCAATATGAGAGCGGCGGCGCTTGTCTATCCGACACTTGTG 1140
Db      ||| 1081 GATTAGGAGAAACAAGCTCTGCAATATGAGAGCGGCGGCGCTTGTCTATCCGACACTTGTG 1140
Qy      ||| 1141 CAGTGGCTTTATGTGCTGATTAATTTGGGCTGTCAAGCCCGCAATGGGAATAGAAGTGG 1200
Db      ||| 1141 CAGTGGCTTTATGTGCTGATTAATTTGGGCTGTCAAGCCCGCAATGGGAATAGAAGTGG 1200
Qy      ||| 1201 TGATGAGGCAAGATATCTTTTGAGAGCAAGAACTACCATTTAGTGAATGAAAACCTTCGATC 1260
Db      ||| 1201 TGATGAGGCAAGATATCTTTTGAGAGCAAGAACTACCATTTAGTGAATGAAAACCTTCGATC 1260
Qy      ||| 1261 CTTTACCTGATTAATTTGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGCAACAAAGTGTAA 1320
Db      ||| 1261 CTTTACCTGATTAATTTGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGCAACAAAGTGTAA 1320
Qy      ||| 1321 TGGCAAGCGTGCAGAGTTCAAGAGAGAGAGCTTCAGATATACCTTCATTTGACAAACA 1380
Db      ||| 1321 TGGCAAGCGTGCAGAGTTCAAGAGAGAGAGCTTCAGATATACCTTCATTTGACAAACA 1380
Qy      ||| 1381 CTGACATACCAAGGATTAAGAAAGAGATTTAACTCTGTATGCTTAAACCTTCCCAACG 1440
Db      ||| 1381 CTGACATACCAAGGATTAAGAAAGAGATTTAACTCTGTATGCTTAAACCTTCCCAACG 1440
Qy      ||| 1441 TCACCAAGGATTAAGAGGATTAACCTTCTTCTTAAAGAGAGAGTGTAAATACCTTC 1500
Db      ||| 1441 TCACCAAGGATTAAGAGGATTAACCTTCTTCTTCTTAAAGAGAGTGTAAATACCTTC 1500
Qy      ||| 1501 TAAAGACTTTGGGACCTCATGATTAATCTTCCAAATCTGTCCCACTCAATGCTTAATCTC 1560
Db      ||| 1501 TAAAGACTTTGGGACCTCATGATTAATCTTCCAAATCTGTCCCACTCAATGCTTAATCTC 1560
Qy      ||| 1561 TAAAGATGATGATGATCAAAACCTTCGCACTTTAATGAAAAACCTTCGCGGCAAGAA 1620
Db      ||| 1561 TAAAGATGATGATGATCAAAACCTTCGCACTTTAATGAAAAACCTTCGCGGCAAGAA 1620
Qy      ||| 1621 GTTCACTGGGCTTGGCAGCTTCTCATATATGTTTTTTTGTGATAGAATGCAAAAGTTG 1680
Db      ||| 1621 GTTCACTGGGCTTGGCAGCTTCTCATATATGTTTTTTTGTGATAGAATGCAAAAGTTG 1680
Qy      ||| 1681 CTGCTTGATCTGAAAAATAAATATATAGTCTGACACTG 1721

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Db      1681 CTGCTTGATCTGAAAAATAAATATATATAGTCTGACACTG 1721
RESULT 4
AAZ33290
ID      AAZ33290 standard; cDNA; 1721 BP.
XX
AC      AAZ33290;
XX
DT      21-FEB-2000 (first entry)
XX
DE      Human heparanase nucleotide sequence.
XX
KW      Human; heparanase; hpa; diagnosis; therapy; tumour; cytostatic;
KW      antidiabetic; immunomodulatory; anti-inflammatory; nephrotropic;
KW      metastasis; adenocarcinoma; squamous cell carcinoma; teratocarcinoma;
KW      mesothelioma; melanoma; lymphoma; leukemia; cancer; sepsis; diabetes;
KW      autoimmune disease; antineoplastic; kidney disease; da.
XX
OS      Homo sapiens.
XX
FH      Key
FT      CDS
FT      Location/Qualifiers
FT      /tag= a
FT      /product= "heparanase"
XX
PN      M09957153-A1.
XX
PD      11-NOV-1999.
XX
PF      29-APR-1999; 99WO-US009255.
XX
PR      01-MAY-1998; 98US-00071739.
XX
PA      (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA      (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA      (FRIE/) FRIEDMAN M M.
XX
PI      Pecker I, Vlodavsky I, Friedman Y, Peretz T;
XX
DR      WPI; 2000-052944/04.
XX
DR      P-PSDB; AAY52990.
XX
PT      Heparanase-specific molecular probes useful for diagnosis and treatment,
PT      e.g. of tumors, and for targeted drug delivery.
XX
PS      Example; Page 82-84; 90pp; English.
XX
CC      The present invention describes heparanase-specific molecular probes,
CC      useful for methods of detecting heparanase in situ. The probes and anti-
CC      heparanase antibodies are used to detect or quantify the expression of
CC      heparanase, for diagnosis and monitoring of diseases (especially
CC      metastasis), for treatment of heparanase-associated diseases (e.g.
CC      tumours, (adeno)carcinoma, squamous cell carcinoma, teratocarcinoma,
CC      mesothelioma, melanoma, lymphoma or leukemia, a solid cancer (or its
CC      metastases) derived from liver, prostate, bladder, breast, ovary, cervix,
CC      colon, skin, intestine, stomach, uterus and pancreas, kidney disease,
CC      diabetes and inflammation, haemorrhagic nephritis, nephrotic syndrome,
CC      sepsis and inflammatory or autoimmune diseases), for targeted drug
CC      delivery (e.g. of anticancer agents) and as research reagents. The
CC      present sequence encodes human heparanase, which is used in the
CC      exemplification of the present invention
XX
SQ      Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;
Query Match 100.0%; Score 1721; DB 3; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 CTAGAGCTTTCGACTCTCCGCTGCGCGGCAAGCTGCGCGGGGAGACAGCAGGTGAGCCCA 60
Db      1 CTAGAGCTTTCGACTCTCCGCTGCGCGGCAAGCTGCGCGGGGAGACAGCAGGTGAGCCCA 60

```

[illegible]

QY	1141	CAGTCGCTTATATGTGGCTGGATTAATTGGCGCTGTCAAGCCGATGGAAATGAGAGTGG	1200
Db	1141	CAGTCGCTTATATGTGGCTGGATTAATTGGCGCTGTCAAGCCGATGGAAATGAGAGTGG <th>1200</th>	1200
QY	1201	TGATGAGGCAAGTATTCTTTGGAGCAGGAAATCACCATTTAGTGGATGAAACTTCGATC <th>1260</th>	1260
Db	1201	TGATGAGGCAAGTATTCTTTGGAGCAGGAAATCACCATTTAGTGGATGAAACTTCGATC <th>1260</th>	1260
QY	1261	CTTTACCTGATTAATTGGCTATCTTCTGTCTCAAGAAATTTGATGGGACCAAGGTGTAA <th>1320</th>	1320
Db	1261	CTTTACCTGATTAATTGGCTATCTTCTGTCTCAAGAAATTTGATGGGACCAAGGTGTAA <th>1320</th>	1320
QY	1321	TGGCAGGCGTGAAGGTTCAAGAGAAAGAAAGCTTCGATATACCTTCATTGCAACAACA <th>1380</th>	1380
Db	1321	TGGCAGGCGTGAAGGTTCAAGAGAAAGAAAGCTTCGATATACCTTCATTGCAACAACA <th>1380</th>	1380
QY	1381	CTGACATCCAAAGTATTAAGAAGAGATTAACTCTGATAGCCATTAACCTCATACG <th>1440</th>	1440
Db	1381	CTGACATCCAAAGTATTAAGAAGAGATTAACTCTGATAGCCATTAACCTCATACG <th>1440</th>	1440
QY	1441	TCAACCAATTAATTCGGGTTACCTTATCCTTTTTCACAGCAAGTGATTAATACCTTC <th>1500</th>	1500
Db	1441	TCAACCAATTAATTCGGGTTACCTTATCCTTTTTCACAGCAAGTGATTAATACCTTC <th>1500</th>	1500
QY	1501	TAAAGCCTTGGGACCTCATGATTAACCTTCACAAATGTGCCAATCATATGCTTACCTC <th>1560</th>	1560
Db	1501	TAAAGCCTTGGGACCTCATGATTAACCTTCACAAATGTGCCAATCATATGCTTACCTC <th>1560</th>	1560
QY	1561	TAAACATGTGTGATGATCAAACTTGGCACTTTTAAATGAAAAAACCCTCCGGCAGGAA <th>1620</th>	1620
Db	1561	TAAACATGTGTGATGATCAAACTTGGCACTTTTAAATGAAAAAACCCTCCGGCAGGAA <th>1620</th>	1620
QY	1621	GTTCACTGGGCTTGCACGCTTTCATATATATGTTTTTTTGTGATAGAAAAATGCCAAAGTTG <th>1680</th>	1680
Db	1621	GTTCACTGGGCTTGCACGCTTTCATATATATGTTTTTTTGTGATAGAAAAATGCCAAAGTTG <th>1680</th>	1680
QY	1681	CTGCTTGATCTGAAATTAATAATATATCTAGTCTGACACTG <th>1721</th>	1721
Db	1681	CTGCTTGATCTGAAATTAATAATATATCTAGTCTGACACTG <th>1721</th>	1721
RESULT 5			
ID	AAA91112	standard; DNA; 1721 BP.	
AC	AAA91112;		
XX			
DT	20-APR-2001	(first entry)	
DE		Human heparanase, coding sequence fragment isolated from EST clone.	
KX		Heparanase; hnp1; wound healing; angiogenesis; restenosis; Scrape;	
KW		atherosclerosis; inflammation; pulmonary disease; Alzheimer's disease;	
RW		neurodegenerative disease; Creutzfeldt-Jakob disease; viral infection;	
XX		gene therapy; mouse; expressed sequence tag; ds.	
OS		Homo sapiens.	
XX			
FN	MO200100643-A2.		
PD	04-JAN-2001.		
PF	19-JUN-2000; 2000MO-IL000358.		
PR	25-JUN-1999; 99US-0140801P.		
XX			
XX		(INSI-) INSIGHT STRATEGY & MARKETING LTD.	
PA		Pecker I, Michal I, Itzhaki H;	
PI			
XX			
DR	WPI; 2001-137930/14.		
XX			
DT		New polynucleotides and polypeptides that are distantly homologous to	

Db 1361 CTGACAAATCCAAAGATATAAGAGAGATTAACTGTGATGCCATTAACCTCCATTAACG 1440
Qy 1441 TCACCAAGTACTGGGGTTACCCCTATCCTTTTCTTAACAAGAAATGATTAATCCTTC 1500
Db 1441 TCACCAAGTACTGGGGTTACCCCTATCCTTTTCTTAACAAGAAATGATTAATCCTTC 1500
Qy 1501 TAAAGACTTGGGAGCCTCATGATTAATCTTCCAAATCTGTCCAACTCAATGGTCTACTC 1560
Db 1501 TAAAGACTTGGGAGCCTCATGATTAATCTTCCAAATCTGTCCAACTCAATGGTCTACTC 1560
Qy 1561 TAAAGATGTGGATGATCAAAACCTTGCCACCTTTAATGAAAAACCTCTCCGGCAGGAA 1620
Db 1561 TAAAGATGTGGATGATCAAAACCTTGCCACCTTTAATGAAAAACCTCTCCGGCAGGAA 1620
Qy 1621 GTTCACTGGGCTGGCAGCTTCTCATATAGTTTTTTGTGATAGAATAAGCAAGTTG 1680
Db 1621 GTTCACTGGGCTGGCAGCTTCTCATATAGTTTTTTGTGATAGAATAAGCAAGTTG 1680
Qy 1681 CTGCTTGATCTGAATAATAATATATAGTCTGACACTG 1721
Db 1681 CTGCTTGATCTGAATAATAATATATAGTCTGACACTG 1721

RESULT 7
ADG88799
ID ADG88799 standard; cDNA; 1721 BP.
XX
AC ADG88799;
XX

DT 11-MAR-2004 (first entry)
XX

DE Human hpa cDNA.
XX

KM Wound healing; heparanase; ulcer; burn; laceration; surgical incision;
KW necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy;
KV gene; ss.
XX

OS Homo sapiens.
XX

XX Key Location/Qualifiers
FH CDS 63..1694
FT /*tag= a
FT /product= "Human hpa protein"
XX

XX US2003161823-A1.
XX

XX 28-AUG-2003.
XX

XX 14-JAN-2003; 2003US-00341582.
XX

XX 31-AUG-1998; 98MO-US017954.
XX

XX 01-MAR-1999; 99US-00258892.
XX

XX 06-FEB-2001; 2001US-0076874.
XX

XX 05-SEP-2001; 2001MO-IL000830.
XX

XX 19-NOV-2001; 2001US-00988113.
XX

XX (ILAN/) ILAN N.
XX

XX (VLAD/) VLADAVSKY I.
XX

XX (YACO/) YACOBY-ZEEVI O.
XX

XX (PECK/) PECKER I.
XX

XX (FEIN/) FEINSTEIN E.
XX

XX Ilan N, Vladavsky I, Yacoby-Zeevi O, Pecker I, Feinstein E;
XX MPI; 2003-897910/82.
XX P-PSDB; ADG88800.
XX
XX Composition for treating a wound comprising recombinant heparanase is
XX PT useful to induce or accelerate wound healing and induce or accelerate
XX PT angiogenesis.
XX
XX Claim 4; SEQ ID NO 9; 143bp; English.
XX

XX The present invention relates to methods and compositions for inducing
CC and/or accelerating wound healing via the catalytic activity of
CC heparanase. The invention is used to induce or accelerate a healing
CC process, particularly of an ulcer, burn, laceration, surgical incision,
CC necrosis, pressure wound, diabetic ulcer and to induce or accelerate
CC angiogenesis. The present sequence is human hpa cDNA.
XX
SQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match 100.0%; Score 1721; DB 10; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAGAGCTTTGAGCTCTCCGCTGCGGCGAGCTGCGGGGGAGACAGCAGGTAGGCCA 60
Db 1 CTAGAGCTTTGAGCTCTCCGCTGCGGCGAGCTGCGGGGGAGACAGCAGGTAGGCCA 60
Qy 61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCTGATGCTGCTCTGGGGC 120
Db 61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCTGATGCTGCTCTGGGGC 120
Qy 121 CGTGGGTCCTCTCTCCCTGCGCGCTGCGCGCGCTGCGCGAGCTGCGAGCTGCTG 180
Db 121 CGTGGGTCCTCTCTCCCTGCGCGCTGCGCGCGCTGCGCGAGCTGCGAGCTGCTG 180
Qy 121 CGTGGGTCCTCTCTCCCTGCGCGCTGCGCGCGCTGCGCGAGCTGCGAGCTGCTG 180
Db 121 CGTGGGTCCTCTCTCCCTGCGCGCTGCGCGCGCTGCGCGAGCTGCGAGCTGCTG 180
Qy 181 ACCTGGACTTGTACCCAGAGGCGCTGACCTGAGTGGCCCTGCTCTGTCGCGCA 240
Db 181 ACCTGGACTTGTACCCAGAGGCGCTGACCTGAGTGGCCCTGCTCTGTCGCGCA 240
Qy 241 CCATTGACGCCAAGCTGCGCAGGACCGCGCTTCTCATCTCTGGGTTCTCCAAAGC 300
Db 241 CCATTGACGCCAAGCTGCGCAGGACCGCGCTTCTCATCTCTGGGTTCTCCAAAGC 300
Qy 241 CCATTGACGCCAAGCTGCGCAGGACCGCGCTTCTCATCTCTGGGTTCTCCAAAGC 300
Db 241 CCATTGACGCCAAGCTGCGCAGGACCGCGCTTCTCATCTCTGGGTTCTCCAAAGC 300
Qy 301 TTGCTACTTGGCCAGAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 301 TTGCTACTTGGCCAGAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Qy 361 ACTTCTTAATTTTGATCCCAAGAGATCACTTTGAAAGAGAAATTAATGAGCAAT 420
Db 361 ACTTCTTAATTTTGATCCCAAGAGATCACTTTGAAAGAGAAATTAATGAGCAAT 420
Qy 421 CTCAAGTCAACCAAGATTTTGGCAATATGAGATCATCTCTGATGTGAGAGAAAGT 480
Db 421 CTCAAGTCAACCAAGATTTTGGCAATATGAGATCATCTCTGATGTGAGAGAAAGT 480
Qy 481 TAGGTTGGAATGGCCCTTACAGAGCAATTTCTTCCAGAACCTAACCAAGAAAGT 540
Db 481 TAGGTTGGAATGGCCCTTACAGAGCAATTTCTTCCAGAACCTAACCAAGAAAGT 540
Qy 541 TCAAGAACAGCACTTACAGAGCAATTTCTTCCAGAACCTAACCAAGAAAGT 600
Db 541 TCAAGAACAGCACTTACAGAGCAATTTCTTCCAGAACCTAACCAAGAAAGT 600
Qy 601 CAGAGCTGACTGATCTTTGGCTTAATGCTTAATGAACACAGATTTGCAAGTGA 660
Db 601 CAGAGCTGACTGATCTTTGGCTTAATGCTTAATGAACACAGATTTGCAAGTGA 660
Qy 661 ACAGTTCTAATGCTCAAGTGTCTCTGAGCTAATGCTCTTCCAGAGGATTAATCTT 720
Db 661 ACAGTTCTAATGCTCAAGTGTCTCTGAGCTAATGCTCTTCCAGAGGATTAATCTT 720
Qy 721 GGGAACTAGGAATGAACCTTAAGCTTTCTTAAGAGGCTGATTTTCAATAGGCT 780
Db 721 GGGAACTAGGAATGAACCTTAAGCTTTCTTAAGAGGCTGATTTTCAATAGGCT 780
Qy 781 CGCAGTTAGAGAGATTAATTAATGCAATTAATCTTAAGAGGCTCACTTCAAAA 840
Db 781 CGCAGTTAGAGAGATTAATTAATGCAATTAATCTTAAGAGGCTCACTTCAAAA 840
Qy 841 ATGCAAACTTATGCTGCTGATGTTGGTCAAGCTTCAAGAAAGACGGCTAAGTCTGA 900
Db 841 ATGCAAACTTATGCTGCTGATGTTGGTCAAGCTTCAAGAAAGACGGCTAAGTCTGA 900


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QY 901 AGAGCTTCCTGAAGGCTGGTGGAGAGATTTGATTGATTCATATGCGATCTACTATTT 960
DB 901 AGAGCTTCCTGAAGGCTGGTGGAGAGATTTGATTGATTCATATGCGATCTACTATTT 960
QY 961 TGAATGACGACGTCTCTACCAAGGAGATTTTCTTAAACCTGATGTAATGGACATTTT 1020
DB 961 TGAATGACGACGTCTCTACCAAGGAGATTTTCTTAAACCTGATGTAATGGACATTTT 1020
QY 1021 TTTCACTGTGTCAAAAAGTTTTCAGAGGTGGTGGAGACCAAGGCTGGCAAGAGTCT 1080
DB 1021 TTTCACTGTGTCAAAAAGTTTTCAGAGGTGGTGGAGACCAAGGCTGGCAAGAGTCT 1080
QY 1081 GGTTCAGGAAACCAAGCTCTGCATATGAGGCGAGGCGCTTGTCTATCCGACACCTTGG 1140
DB 1081 GGTTCAGGAAACCAAGCTCTGCATATGAGGCGAGGCGCTTGTCTATCCGACACCTTGG 1140
QY 1141 CAGCTGGCTTTATGTGGCTGGATTAATTTGGGCTGTCTACGCCGAAATGGGAATGAAGTG 1200
DB 1141 CAGCTGGCTTTATGTGGCTGGATTAATTTGGGCTGTCTACGCCGAAATGGGAATGAAGTG 1200
QY 1201 TGATGAGGCAAGTATTTCTTTGAGCAGGAATACCACTTATGATGTAAGTAACTTCGATC 1260
DB 1201 TGATGAGGCAAGTATTTCTTTGAGCAGGAATACCACTTATGATGTAAGTAACTTCGATC 1260
QY 1261 CTTTACCTGATTTATTTGGCTATCTCTTCTGTCAAGAAATTTGGTGGCAACCAAGTGTAA 1320
DB 1261 CTTTACCTGATTTATTTGGCTATCTCTTCTGTCAAGAAATTTGGTGGCAACCAAGTGTAA 1320
QY 1321 TGGCAAGCGTGCAGAGGTTCAAGAGAGAAAGCTTGAATATACCTTCATTCGACAAACA 1380
DB 1321 TGGCAAGCGTGCAGAGGTTCAAGAGAGAAAGCTTGAATATACCTTCATTCGACAAACA 1380
QY 1381 CTGACATCCAGATTAAGATTAAGAGAGATTTAACTCTGTATGCCATTAACCTCCATTAACG 1440
DB 1381 CTGACATCCAGATTAAGATTAAGAGAGATTTAACTCTGTATGCCATTAACCTCCATTAACG 1440
QY 1441 TCACCAAGTACTTGGGTTACCTTATCTTTTCTTACAGAGATGATTAATTAATCTTTC 1500
DB 1441 TCACCAAGTACTTGGGTTACCTTATCTTTTCTTACAGAGATGATTAATTAATCTTTC 1500
QY 1501 TAAAGCTTTGGGACCTCATGATTAATCTTCCAAATCTGTCCAACTCAATGCTTAACTC 1560
DB 1501 TAAAGCTTTGGGACCTCATGATTAATCTTCCAAATCTGTCCAACTCAATGCTTAACTC 1560
QY 1561 TAAAGATGATGATGATCAAACTTGCACCTTTAAATGAGAAACCTTCCGCGCAGGAA 1620
DB 1561 TAAAGATGATGATGATCAAACTTGCACCTTTAAATGAGAAACCTTCCGCGCAGGAA 1620
QY 1621 GTTCACTGGGCTTCCAGCTTCTCATATAGTTTTTTTGTGATTAAGAAATGCGCAAGTTG 1680
DB 1621 GTTCACTGGGCTTCCAGCTTCTCATATAGTTTTTTTGTGATTAAGAAATGCGCAAGTTG 1680
QY 1681 CTGCTTGATCTGAATAATTAATAATATACATAGCCGACACG 1721
DB 1681 CTGCTTGATCTGAATAATTAATAATATACATAGCCGACACG 1721

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RESULT 8
ID ADL16380 standard; cDNA; 1721 BP.

ADL16380;

06-MAY-2004 (first entry)

Human heparanase partial cDNA #2.

Human; ss; heparanase; gene; heparanase-dependent cancer; cancer;

autoimmune reaction; inflammation; chromosome 4.

OS Homo sapiens.

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PN US2003236215-A1.
XX
XX 25-DEC-2003.
PD
XX
PF 09-JUN-2003; 2003US-00456573.
XX
XX 31-AUG-1998; 98WO-US017954.
PR 01-MAR-1999; 99US-00258892.
PR 08-NOV-1999; 99US-00435739.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX (HADA-) HADASTI MEDICAL RES SERVICES & DEV.
XX
XX Pecker I, Vlodavsky I, Feinstein E;
XX WPI; 2004-070610/07.
XX
XX New antisense oligonucleotide hybridizable with a polynucleotide encoding
XX a polypeptide with heparanase activity, useful for treating diseases such
XX as cancer and autoimmune disorders.
XX
XX Example 1; SEQ ID NO 11; 108bp; English.
XX
XX The invention relates to an antisense oligonucleotide (ASO) comprising a
XX polynucleotide or a polynucleotide analogue of at least 10 bases being
XX hybridizable in vivo, under physiological conditions, with a portion of
XX a polynucleotide strand encoding a polypeptide having heparanase
XX catalytic activity. Also included are a method of in vivo downregulating
XX heparanase activity (comprising administering the ASO in vivo), a method
XX of treating a subject suffering from a pathological condition
XX (characterised by heparanase activity, comprising administering ASO to
XX the subject), a pharmaceutical composition comprising the ASO and a
XX carrier, an antisense nucleic acid construct (comprising the ASO and a
XX sequence and a polynucleotide sequence directing the synthesis of an
XX antisense RNA sequence of at least 10 bases being hybridizable in vivo,
XX under physiological conditions, with a polynucleotide strand encoding a
XX polypeptide having heparanase catalytic activity), a method of in vivo
XX downregulating heparanase activity (comprising administering in vivo the
XX antisense nucleic acid construct), a pharmaceutical composition
XX comprising the antisense nucleic acid construct and a carrier, and an
XX analogue of at least 10 bases being hybridizable in vivo, under
XX physiological conditions, with a portion of a polynucleotide strand being
XX characterised by forming at least a portion of an untranslated region
XX (UTR) for a polynucleotide strand encoding a polypeptide having
XX heparanase catalytic activity. The methods and compositions of the
XX present invention are useful for the prevention and/or treatment of
XX diseases or conditions associated with aberrant heparanase activity, such
XX as heparanase-dependent cancer, cancer, autoimmune reaction and
XX inflammation. The gene for human heparanase is located on chromosome 4.
XX The present sequence is a human heparanase cDNA.
XX
SQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

```

Query Match 100.0%; Score 1721; DB 12; Length 1721;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CTAGAGCTTTGCACTCCGCTGGCGGAGCTGGGCGGAGGAGCGACCAAGTGAACCCA 60
DB 1 CTAGAGCTTTGCACTCCGCTGGCGGAGCTGGGCGGAGGAGCGACCAAGTGAACCCA 60
QY 61 AGATGCTGCTGCGCTGGAACCTGCGCTCGCGCGCGCTGATGCTGCTCTCTGGGGC 120
DB 61 AGATGCTGCTGCGCTGGAACCTGCGCTCGCGCGCGCTGATGCTGCTCTCTGGGGC 120
QY 121 CGCTGGGTCCCTCTCCGCTGGGCGCGCTGGCGGAGCTGCGGAGCAAGAGAGCTGTGG 180
DB 121 CGCTGGGTCCCTCTCCGCTGGGCGCGCTGGCGGAGCTGCGGAGCAAGAGAGCTGTGG 180
QY 181 ACCTGACCTTCTTACCAAGAGCGCTGCACTGTGAGCCCTGTCTCTGTCGCTCA 240
DB 181 ACCTGACCTTCTTACCAAGAGCGCTGCACTGTGAGCCCTGTCTCTGTCGCTCA 240

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OY	241	CCATTGAGCCAAACCTGGCCACACGACCCGGCTTCTCATCTCTGGGTTCTCCAAAGC	300
Db	241	CCATTGAGCCAAACCTGGCCACACGACCCGGCTTCTCATCTCTGGGTTCTCCAAAGC	300
OY	301	TTTCGTACTTGGCCACGAGGCTTGTCTCTCGCTACTCTAGGTTTGTGTGACCAAGACG	360
Db	301	TTTCGTACTTGGCCACGAGGCTTGTCTCTCGGTACTCTAGGTTTGTGTGACCAAGACG	360
OY	361	ACTTCTTAATTTTGCATCCCAAGAAAGAAATCAACTTTGAAGAGAAAGTTACTGCAAT	420
Db	361	ACTTCTTAATTTTGCATCCCAAGAAAGAAATCAACTTTGAAGAGAAAGTTACTGCAAT	420
OY	421	CTCAAGTCAACCAAGGATATTTTGCAATATATGATTCATCCCTCTGATGTGAGAGAAAGT	480
Db	421	CTCAAGTCAACCAAGGATATTTTGCAATATATGATTCATCCCTCTGATGTGAGAGAAAGT	480
OY	481	TACGGTTGAAATGCGCTTACACGAGGACAAATTCCTCCGAGAACACTACCGAAAAAGT	540
Db	481	TACGGTTGAAATGCGCTTACACGAGGACAAATTCCTCCGAGAACACTACCGAAAAAGT	540
OY	541	TCAGAAACAGACCCCTACTCAAGAACCTCTGTAGTGTGTATACCTTTGCAACCTGCT	600
Db	541	TCAGAAACAGACCCCTACTCAAGAACCTCTGTAGTGTGTATACCTTTGCAACCTGCT	600
OY	601	CAGACTGGAATTTGATCTTTTGCCCTTAATGCTTTATTAAGAACACAGATTTTGCAGTGA	660
Db	601	CAGACTGGAATTTGATCTTTTGCCCTTAATGCTTTATTAAGAACACAGATTTTGCAGTGA	660
OY	661	ACAGTTCTTAATGCTCAAGTTGCTCTCTGCACTACTGCTCTTCCAGGGGTTATCAATTTCTT	720
Db	661	ACAGTTCTTAATGCTCAAGTTGCTCTCTGCACTACTGCTCTTCCAGGGGTTATCAATTTCTT	720
OY	721	GGAACCTAGGCAATGAACCTAACAGTTTCCCTTAAGAAAGGCTGATATTTTTCATCAATGGGT	780
Db	721	GGAACCTAGGCAATGAACCTAACAGTTTCCCTTAAGAAAGGCTGATATTTTTCATCAATGGGT	780
OY	781	CGCAGTTAGGAGAGATTATATTCATATGTCATTAACCTTTGAAGAAAGTCCACTTCAAAA	840
Db	781	CGCAGTTAGGAGAGATTATATTCATATGTCATTAACCTTTGAAGAAAGTCCACTTCAAAA	840
OY	841	ATGCAAACTCTAATGCTCTCTGATGTTTGGTCAAGCTCCGAAAGAACCGCTAAGATGCTGA	900
Db	841	ATGCAAACTCTAATGCTCTCTGATGTTTGGTCAAGCTCCGAAAGAACCGCTAAGATGCTGA	900
OY	901	AGAGCTTCTCTGAAGGCTGGTGAGAAAGTATGATTCAAGTTACATGCACTCACTATAT	960
Db	901	AGAGCTTCTCTGAAGGCTGGTGAGAAAGTATGATTCAAGTTACATGCACTCACTATAT	960
OY	961	TGAATGACACGACTGCTACACAGGGAAGATTTTCTAAACCTCTGATATATTTGAATTTT	1020
Db	961	TGAATGACACGACTGCTACACAGGGAAGATTTTCTAAACCTCTGATATATTTGAATTTT	1020
OY	1021	TTTCATCTGTGCAAAAAGTTTCCAGGAGGTTGAGAGACACAGGCTGGCAAGAAAGTCT	1080
Db	1021	TTTCATCTGTGCAAAAAGTTTCCAGGAGGTTGAGAGACACAGGCTGGCAAGAAAGTCT	1080
OY	1081	GATTAGAGAAAACAAGCTCTGCATATGAGCGGAGCGCCTTTCGATCCGACACTTTG	1140
Db	1081	GATTAGAGAAAACAAGCTCTGCATATGAGCGGAGCGCCTTTCGATCCGACACTTTG	1140
OY	1141	CAGCTGGCTTTATGAGGCTGGAATAATGGGCTGTCAAGCCCGAATGGGAATAGAAAGTGG	1200
Db	1141	CAGCTGGCTTTATGAGGCTGGAATAATGGGCTGTCAAGCCCGAATGGGAATAGAAAGTGG	1200
OY	1201	TGATAGGCAAGATATTTCTTTGAGCAGGAACTACACTTTAGTGAATGAAAATTCTGCATC	1260
Db	1201	TGATAGGCAAGATATTTCTTTGAGCAGGAACTACACTTTAGTGAATGAAAATTCTGCATC	1260
OY	1261	CTTTACCTGATTAATGGGCTATCTCTTCTGTCTAAGAAATTTGGTGGCACCAAGAGTTTAA	1320
Db	1261	CTTTACCTGATTAATGGGCTATCTCTTCTGTCTAAGAAATTTGGTGGCACCAAGAGTTTAA	1320

QY	1321	TGGCAGGTCGCAAGTTCAAAGAAGAAAGAACCTTGCATGTACTCCATTGCGCAACA	1380
Dd	1321	TGGCAAGGTGCCAAGTTCAAAGAAGAAAGACCTTGAGTAATCCCTCATTTGCAACA	1380
QY	1381	CTGACAAATCCAAGGTTAAAGAAAGAGATTAACTCTGTATGCATATAAACCCTCATACG	1440
Dd	1381	CTGACAAATCCAAGGTTAAAGAAAGAGATTAACTCTGTATGCCATATAAACCCTCATACG	1440
QY	1441	TCACCAAGTACTTGGCGTTACCCCTATCTTTTTTGAACAAGCAAGTGATTAATACCTTC	1500
Dd	1441	TCACCAAGTACTTGGCGTTACCCCTATCTTTTTTGAACAAGCAAGTGATTAATACCTTC	1500
QY	1501	TAAAGCCTTTGGGACCTCANTGATTACTTTTCCAATCTGTCCAACCTAAATGCTTAATCT	1560
Dd	1501	TAAAGCCTTTGGGACCTCANTGATTACTTTTCCAATCTGTCCAACCTCAATGCTTAATCT	1560
QY	1561	TAAAGATGTTGAGATGATCAAAACCTTGCCACTTTAATGAAAACCTCTCGGCGCAGGAA	1620
Dd	1561	TAAAGATGTTGAGATGATCAAAACCTTGCCACTTTAATGAAAACCTCTCCGCGCACGAA	1620
QY	1621	GTTCACTGGGCTTGGCAGCTTTCTCATATAGTTTTTTTGTGATTAAGAAATGCCAAAGTTG	1680
Dd	1621	GTTCACTGGGCTTGGCAGCTTTCTCATATAGTTTTTTTGTGATTAAGAAATGCCAAAGTTG	1680
QY	1681	CTGCTTGATCTGAAAAATAAATATATCAATAGCTCGACACTG 1721	
Dd	1681	CTGCTTGATCTGAAAAATAAATATATCAATAGCTCGACACTG 1721	

CC	The invention relates to an antisense oligonucleotide (ASO) comprising a
XX	
PS	Claim 2; SEQ ID NO 9; 108bp; English.
PT	
TX	
PR	a polypeptide with heparanase activity, useful for treating diseases such
PT	as cancer and autoimmune disorders.
XX	
PA	(INSI-) INSIGHT STRATEGY & MARKETING LTD.
XX	(HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX	
PI	Pecker I, Vlodavsky I, Feinstein E;
XX	
DR	WPI; 2004-070610/07.
XX	
PT	New antisense oligonucleotide hybridizable with a polynucleotide encoding
XX	
AC	ADL16378;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Human heparanase partial cDNA #1.
XX	
KW	Human; ss; heparanase; gene; heparanase-dependent cancer; cancer;
XX	autimmune reaction; inflammation; chromosome 4.
OS	Homo sapiens.
XX	
FH	Key location/Qualifiers
FT	3'UTR 1695..1721
FT	/tag= a
FT	/note= "Claimed in claim 20"
XX	
PN	US2003236215-A1.
XX	
PD	25-DEC-2003.
XX	
PF	09-JUN-2003; 2003US-00456573.
XX	
PR	31-AUG-1998; 98WO-US01795&.
PR	01-MAR-1999; 99US-00258892.
XX	
PR	08-NOV-1999; 99US-00435739.
XX	
XX	
ADL16378	standard; cDNA; 1721 BP.
RESULT 9	

CC polynucleotide or a polynucleotide analogue of at least 10 bases being
CC hybridizable in vivo, under physiological conditions, with a portion of
CC a polynucleotide strand encoding a polypeptide having heparanase
CC catalytic activity. Also included are a method of in vivo downregulating
CC heparanase activity (comprising administering the ASO in vivo), a method
CC of treating a subject suffering from a pathological condition
CC (characterized by heparanase activity, comprising administering ASO to
CC the subject), a pharmaceutical composition comprising the ASO and a
CC carrier, an antisense nucleic acid construct (comprising the ASO and a
CC sequence and a polynucleotide sequence directing the synthesis of an
CC antisense RNA sequence of at least 10 bases being hybridizable in vivo,
CC under physiological conditions, with a polynucleotide strand encoding a
CC polypeptide having heparanase catalytic activity), a method of in vivo
CC downregulating heparanase activity (comprising administering in vivo the
CC antisense nucleic acid construct), a pharmaceutical composition
CC comprising the antisense nucleic acid construct and a carrier, and an
CC analogue of at least 10 bases being hybridizable in vivo, under
CC physiological conditions, with a portion of a polynucleotide strand being
CC characterized by forming at least a portion of an untranslated region
CC heparanase catalytic activity. The methods and compositions of the
CC present invention are useful for the prevention and/or treatment of the
CC diseases or conditions associated with aberrant heparanase activity, such
CC as heparanase-dependent cancer, cancer, autoimmune reaction and
CC inflammation. The gene for human heparanase is located on chromosome 4.
CC
CC
XX
SQ

Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match 100.0%; Score 1721; DB 12; Length 1721;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGAGCTTTCGACTCTCCGCTGCGGCGAGCTGCGGCGGAGAGCAGCAGGCTGAGCCCA 60
Db 1 CTAGAGCTTTCGACTCTCCGCTGCGGCGAGCTGCGGCGGAGAGCAGCAGGCTGAGCCCA 60
QY 61 AGATGCTGCTGCGCTCGAAGCCTGCGCTCGCGCGCGCGCTGATGCTGCTGCTGCGGCG 120
Db 61 AGATGCTGCTGCGCTCGAAGCCTGCGCTCGCGCGCGCGCTGATGCTGCTGCTGCGGCG 120
QY 121 CGCTGGGTGCGCTGCGCTGCGGCGCGCTGCGGCGCGCTGATGCTGCTGCTGCGGCG 180
Db 121 CGCTGGGTGCGCTGCGCTGCGGCGCGCTGCGGCGCGCTGATGCTGCTGCTGCGGCG 180
QY 181 ACCTGACTTCTTCAACCCAGAGCGCGTGCACCTGCTGAGCGCCCTGCTGCTGCTGCA 240
Db 181 ACCTGACTTCTTCAACCCAGAGCGCGTGCACCTGCTGAGCGCCCTGCTGCTGCTGCA 240
QY 241 CCATTGAGCGCCCACTGCGCAGCAGACCGCGGTTCTCATCTCTGAGTTTCCCAAGC 300
Db 241 CCATTGAGCGCCCACTGCGCAGCAGACCGCGGTTCTCATCTCTGAGTTTCCCAAGC 300
QY 301 TTTCGATCTTGGCGCAGAGGCTTGTCTCTGCTGCTGCTGAGGTTTGGTGCACCAAGC 360
Db 301 TTTCGATCTTGGCGCAGAGGCTTGTCTCTGCTGCTGCTGAGGTTTGGTGCACCAAGC 360
QY 361 ACTTCCTAATTTTGGATCCCAAGAGGATCACTTTGAAGAGAGAGTTACTGGCAAT 420
Db 361 ACTTCCTAATTTTGGATCCCAAGAGGATCACTTTGAAGAGAGAGTTACTGGCAAT 420
QY 421 CTCAAGTCAACAGAGATATTGCAAAATATGATCCATCCCTCTGATGTGAGAGAGT 480
Db 421 CTCAAGTCAACAGAGATATTGCAAAATATGATCCATCCCTCTGATGTGAGAGAGT 480
QY 481 TAGCGTTGGAATGGCCCTTACAGAGCAATTGCTACTCCGAGAACTACAGAAAAAGT 540
Db 481 TAGCGTTGGAATGGCCCTTACAGAGCAATTGCTACTCCGAGAACTACAGAAAAAGT 540
QY 541 TCAAGAACAGACCTTCTCAAGAAAGCTGTGATAGTGTGTATACCTTTTGCAAACTGCT 600
Db 541 TCAAGAACAGACCTTCTCAAGAAAGCTGTGATAGTGTGTATACCTTTTGCAAACTGCT 600

QY 601 CAGGACTGACCTTGAATCTTTGGCCTTAATGAGTTATTAAGAACAGAGATTTGAGTGA 660
Db 601 CAGGACTGACCTTGAATCTTTGGCCTTAATGAGTTATTAAGAACAGAGATTTGAGTGA 660
QY 661 AAGAGTTCTAATGCTGAGTTGCTCCCTGAGCTACCTGCTCTCCCAAGGGTATTAACATTTCT 720
Db 661 AAGAGTTCTAATGCTGAGTTGCTCCCTGAGCTACCTGCTCTCCCAAGGGTATTAACATTTCT 720
QY 721 GGGAACTGAGCAATGAACCTTAACAGTTTCTTAAGAGGCTGATTTTATTAAGAGT 780
Db 721 GGGAACTGAGCAATGAACCTTAACAGTTTCTTAAGAGGCTGATTTTATTAAGAGT 780
QY 781 CGCAGTTGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
Db 781 CGCAGTTGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
QY 841 ATGCAAACTCTATGATGCTGATGTTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 900
Db 841 ATGCAAACTCTATGATGCTGATGTTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 900
QY 901 AGAGCTTCTGAGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Db 901 AGAGCTTCTGAGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
QY 961 TGAATGACCGACTGCTACCAAGGAGATTTTCTAACCCTGATGATGATGATGATGATGAT 1020
Db 961 TGAATGACCGACTGCTACCAAGGAGATTTTCTAACCCTGATGATGATGATGATGATGAT 1020
QY 1021 TTTCATCTGAGCAAAAGTTTTCAGTGTGTTGAGAGCAGCAGGCTGCAAGAGGCT 1080
Db 1021 TTTCATCTGAGCAAAAGTTTTCAGTGTGTTGAGAGCAGCAGGCTGCAAGAGGCT 1080
QY 1081 GGTAGAGAAACAAAGCTCTGCAATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
Db 1081 GGTAGAGAAACAAAGCTCTGCAATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
QY 1141 CAGCTGGCTTTATGTCGCTGATTAATTTGAGCTGTCAGCCGATGAGGAGTGAATGAG 1200
Db 1141 CAGCTGGCTTTATGTCGCTGATTAATTTGAGCTGTCAGCCGATGAGGAGTGAATGAG 1200
QY 1201 TGATGAGCAAGTATCTTTGAGCAGAGAACTACCTTAATGATGATGATGATGATGATG 1260
Db 1201 TGATGAGCAAGTATCTTTGAGCAGAGAACTACCTTAATGATGATGATGATGATGATG 1260
QY 1261 CTTTACCTGATTTATGCTATCTTTCTGTTCAAGAAATTTGAGGAGCAACAGGTTTAA 1320
Db 1261 CTTTACCTGATTTATGCTATCTTTCTGTTCAAGAAATTTGAGGAGCAACAGGTTTAA 1320
QY 1321 TGGCAAGGTCAGAGTTTCAAAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
Db 1321 TGGCAAGGTCAGAGTTTCAAAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
QY 1381 CTGCAATTCAGAGTATTAAGAGAGATTTAATCTGTATGATCCATTAACCTCCATAAG 1440
Db 1381 CTGCAATTCAGAGTATTAAGAGAGATTTAATCTGTATGATCCATTAACCTCCATAAG 1440
QY 1441 TCAACAGTACTTGGCGTTAACCCTATCTTTTCTTAACAAGCAAGTGAATTAATCTTC 1500
Db 1441 TCAACAGTACTTGGCGTTAACCCTATCTTTTCTTAACAAGCAAGTGAATTAATCTTC 1500
QY 1501 TAAGACCTTTGGGACCTCATGATTAATCTTCAAAATCTGTCAAACTCAATGATCTTA 1560
Db 1501 TAAGACCTTTGGGACCTCATGATTAATCTTCAAAATCTGTCAAACTCAATGATCTTA 1560
QY 1561 TAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
Db 1561 TAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1621 GTTCACTGGGCTGCGCACTTCTCATATAGTTTGTGTAAGAAATGCAAAAGTTG 1680
Db 1621 GTTCACTGGGCTGCGCACTTCTCATATAGTTTGTGTAAGAAATGCAAAAGTTG 1680

QY	421	CTCAAGTCAACAGGATATTGTCAAATATGATGATCCATCCCTGTATGTGGAGGAAGT	480
Db	421	CTCAAGTCAACAGGATATTGTCAAATATGATGATCCATCCCTGTATGTGGAGGAAGT	480
QY	481	TACGGTTGGAAATGGCCCTTACACAGAGCAATTGTCTATCCGAGAAACATCTACGAAAAAGT	540
Db	481	TACGGTTGGAAATGGCCCTTACACAGAGCAATTGTCTATCCGAGAAACATCTACGAAAAAGT	540
QY	541	TCAGAAACGACACTTACAGAGGCTGTAGATGTGTATACCTTTTGCAAACTGCT	600
Db	541	TCAGAAACGACACTTACAGAGGCTGTAGATGTGTATACCTTTTGCAAACTGCT	600
QY	601	CAGGACTGGACTTGATCTTTGGCCCTAAATAGCCATTATAGAACACACAGATTTGGAGTGA	660
Db	601	CAGGACTGGACTTGATCTTTGGCCCTAAATAGCCATTATAGAACACACAGATTTGGAGTGA	660
QY	661	ACAGTTCTAATGCTCAGTTGCTCTCGAGACTATGCTCTTCCAAAGGGATTAACATTTCTT	720
Db	661	ACAGTTCTAATGCTCAGTTGCTCTCGAGACTATGCTCTTCCAAAGGGATTAACATTTCTT	720
QY	721	GGGAACTAGGCATGAACTTAACAGTTTCTTAAAGGCTGATATTTTCATCAATGGGT	780
Db	721	GGGAACTAGGCATGAACTTAACAGTTTCTTAAAGGCTGATATTTTCATCAATGGGT	780
QY	781	CGCACTTAGAGAAAGATTATATTCAATTGCAATAAACTTTAAGAAAGTCCACCTTCAAA	840
Db	781	CGCACTTAGAGAAAGATTATATTCAATTGCAATAAACTTTAAGAAAGTCCACCTTCAAA	840
QY	841	ATGCAAAACTCTAATGATGCTGATGTTGGTCACTTCGAAAGAAACGCTGATAGTGTGA	900
Db	841	ATGCAAAACTCTAATGATGCTGATGTTGGTCACTTCGAAAGAAACGCTGATAGTGTGA	900
QY	901	AGAGCTTCTGAAAGCTGTGTGAGAAAGTATGATTCAGATTACATGCACTCACTATTT	960
Db	901	AGAGCTTCTGAAAGCTGTGTGAGAAAGTATGATTCAGATTACATGCACTCACTATTT	960
QY	961	TGAATGAGACGACTGTCTACAGGGAAGATTTTCTAAACCTGATGATTTGGACATTTTTA	1020
Db	961	TGAATGAGACGACTGTCTACAGGGAAGATTTTCTAAACCTGATGATTTGGACATTTTTA	1020
QY	1021	TTTCAATCTGTGCAAAAAGTTTCCAGGTGTTGAGAGCAACGAGGCTGGCAAGAGGCT	1080
Db	1021	TTTCAATCTGTGCAAAAAGTTTCCAGGTGTTGAGAGCAACGAGGCTGGCAAGAGGCT	1080
QY	1081	GTTTAGAGAAACAAGCTCTGCATATGAGCGGAGCGCCCTGTGTAATCCGACACTTGG	1140
Db	1081	GTTTAGAGAAACAAGCTCTGCATATGAGCGGAGCGCCCTGTGTAATCCGACACTTGG	1140
QY	1141	CAGCTGGCTTATGTGGCTGTGATAATTGGGCTGTCAAGCCCGAATGGGAATGAAATGG	1200
Db	1141	CAGCTGGCTTATGTGGCTGTGATAATTGGGCTGTCAAGCCCGAATGGGAATGAAATGG	1200
QY	1201	TGATAGGCAAGTATCTTTTGGAGAGAGAACTTACATTTAGTGATGAAACTTCGATC	1260
Db	1201	TGATAGGCAAGTATCTTTTGGAGAGAGAACTTACATTTAGTGATGAAACTTCGATC	1260
QY	1261	CTTTACTGATTAATTGGCTATCTCTTCTGTCAAGAAATTTGGTGGGACCAAGTGTTAA	1320
Db	1261	CTTTACTGATTAATTGGCTATCTCTTCTGTCAAGAAATTTGGTGGGACCAAGTGTTAA	1320
QY	1321	TGGCAAGCGTGCAGGTTCAAAAGAGAGGATTTAATCTGTATAGCCATTAATCCCTCAATAG	1380
Db	1321	TGGCAAGCGTGCAGGTTCAAAAGAGAGGATTTAATCTGTATAGCCATTAATCCCTCAATAG	1380
QY	1381	CTGAACAATCCAAAGGATTAAGAAAGAGATTTAATCTGTATAGCCATTAATCCCTCAATAG	1440
Db	1381	CTGAACAATCCAAAGGATTAAGAAAGAGATTTAATCTGTATAGCCATTAATCCCTCAATAG	1440
QY	1441	TCACCAAGTACTTGGGTTACCTTATCTTTTCTTAAACAAGCAATGTGATAATCTTTC	1500
Db	1441	TCACCAAGTACTTGGGTTACCTTATCTTTTCTTAAACAAGCAATGTGATAATCTTTC	1500
QY	1501	TAAAGCTTTGGGACCTCAGATTAATTTTCCAAATCTGTCCAATCAATGGTCTTAACTC	1560

Db	1501	TAAAGATGGTGGATGATGATCAAACTTGGCACTTTAATGAAAAA	CCTCTCCGGCCAGAA	1622			
Qy	1561	TAAAGATGGTGGATGATGATCAAACTTGGCACTTTAATGAAAAA	CCTCTCCGGCCAGAA	1622			
Db	1561	TAAAGATGGTGGATGATGATCAAACTTGGCACTTTAATGAAAAA	CCTCTCCGGCCAGAA	1622			
Qy	1621	GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGATAGAAAA	TGCCAAAGTTG	1688			
Db	1621	GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGATAGAAAA	TGCCAAAGTTG	1688			
Qy	1661	CTGCTTGATCTGAAAAATAAATATAGTACTAGTCTGACACTG	1721				
Db	1661	CTGCTTGATCTGAAAAATAAATATAGTACTAGTCTGACACTG	1721				
RESULT 12							
ID	AAK35650	standard; cDNA; 1899 BP.					
AC	AAK35650;						
DT	09-JUL-1999	(first entry)					
DE	cDNA encoding a human heparanase protein.						
KM	Heparanase; hpa; modulator; heparin-binding growth factor;						
KM	cellular response; cytokine; cell interaction; plasma lipoprotein;						
KM	cellular susceptibility; infection; disintegration;						
KM	neurodegenerative plaque; wound healing; angiogenesis; restenosis;						
KM	atherosclerosis; inflammation; neurodegenerative disease; neuritis;						
KM	plasma heparin; micrometastasis; autoimmune lesion; renal failure; ss.						
OS	Homo sapiens.						
XX							
PN	W09911798-A1.						
PD	11-MAR-1999.						
XX							
PF	31-AUG-1998; 98WO-US017954.						
PR	02-SEP-1997; 97US-00922170.						
PR	02-JUL-1998; 98US-00109386.						
XX							
PA	(INSI-) INSIGHT STRATEGY & MARKETING LTD.						
PA	(HADA-) HADASIT MEDICAL RES SERVICES & DEV.						
PA	(FRIE/) FRIEDMAN M M.						
PI	Pecker I, Vlodavsky I, Feinstein E;						
DR	WPI; 1999-302255/25.						
DR	P-PSDB; AAY02346.						
XX							
PT	New human polynucleotide useful for treating angiogenesis, restenosis,						
PT	and inflammation.						
XX							
PS	Claim 4; Page 64-65; 63pp; English.						
XX							
CC	The specification describes a polypeptide having heparanase (hpa)						
CC	activity. The recombinant protein is used as a modulator of heparin-						
CC	binding growth factors, cellular responses to heparin-binding growth						
CC	factors and cytokines, cell interaction with plasma lipoproteins,						
CC	cellular susceptibility to viral, protozoal and bacterial infections or						
CC	disintegration of neurodegenerative plaques. Heparanase may be useful for						
CC	conditions such as wound healing, angiogenesis, restenosis,						
CC	atherosclerosis, inflammation, neurodegenerative diseases, and viral						
CC	infections. Mammalian heparanase can be used to neutralize plasma						
CC	heparin, and anti-heparanase antibodies may be applied for						
CC	immunodetection and diagnosis of micrometastases, autoimmune lesions, and						
CC	renal failure in biopsy specimens, plasma samples, and body fluids. The						
CC	present sequence encodes human heparanase						
XX							
Sequence	1899 BP; 495 A; 433 C; 510 G; 461 T; 0 U; 0 Other;						

Query Match 99.9%; Score 1719.4; DB 2; Length 1899; Best Local Similarity 99.9%; Pred. No. 0; Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CTAGAGCTTTCGACTCTCCGCTGCGGAGCTGGCGGGGAGACAGCAGGTAGGCCA 60
DB 179 CTAGAGCTTTCGACTCTCCGCTGCGGAGCTGGCGGGGAGACAGCAGGTAGGCCA 238
QY 61 AGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 229 AGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 298
QY 121 CGCTGGCTCCCTCTCCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 299 CGCTGGCTCCCTCTCCCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 358
QY 181 ACCGGAAGCTTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB 359 ACCGGAAGCTTTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 418
QY 241 CCATTGAGCGCAACCTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 300
DB 419 CCATTGAGCGCAACCTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 478
QY 301 TTGCTACCTTGGCGCAGGAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 479 TTGCTACCTTGGCGCAGGAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538
QY 361 ACTTCTTAATTTTGCATATCCCAAGAGAGATCAACCTTTGAGAGAGATTTCTGGCAAT 420
DB 539 ACTTCTTAATTTTGCATATCCCAAGAGAGATCAACCTTTGAGAGAGATTTCTGGCAAT 598
QY 421 CTGAATCAACGAGGATTTTGCATATATGATATCAATCCCTCTGATGAGAGAGAT 480
DB 599 CTGAATCAACGAGGATTTTGCATATATGATATCAATCCCTCTGATGAGAGAGAT 658
QY 481 TACGGTTGAGATGAGCCTTCAAGAGAGATTTGCTACTCCAGAGAGATTTGAGAGAG 540
DB 659 TACGGTTGAGATGAGCCTTCAAGAGAGATTTGCTACTCCAGAGAGATTTGAGAGAG 718
QY 541 TCAAGAGAGAGATTTGCTACTCAAGAGAGATTTGCTACTCAAGAGAGATTTGCTACT 600
DB 719 TCAAGAGAGAGATTTGCTACTCAAGAGAGATTTGCTACTCAAGAGAGATTTGCTACT 778
QY 601 CAGGACTGAGCTTGTATCTTTGGCTTAATGAGGATTTTGAAGAGAGATTTGAGAGAG 660
DB 779 CAGGACTGAGCTTGTATCTTTGGCTTAATGAGGATTTTGAAGAGAGATTTGAGAGAG 838
QY 661 ACAATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 839 ACAATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 898
QY 721 GGGAACTAGGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 780
DB 899 GGGAACTAGGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 958
QY 781 CGCAGTTAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
DB 959 CGCAGTTAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1018
QY 841 ATGCAAAATCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 1019 ATGCAAAATCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1078
QY 901 AGAGCTTCTGAGAGGCTGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAAT 960
DB 1079 AGAGCTTCTGAGAGGCTGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAAT 1138
QY 961 TGAATGAGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
DB 1139 TGAATGAGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1198

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QY 1021 TTTCATCTGTGCAAAAAGTTTTCAGAGTGTGAGAGACCAAGGCTGGCAAGAGCTCT 1080
DB 1199 TTTCATCTGTGCAAAAAGTTTTCAGAGTGTGAGAGACCAAGGCTGGCAAGAGCTCT 1258
QY 1081 GGTTAGAGAAAACAAGCTCTGCAATATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
DB 1259 GGTTAGAGAAAACAAGCTCTGCAATATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1318
QY 1141 CAGCTGGCTTATATGAGTGTGATTAATTTGGGCTGTGAGGCTGGAGATGGAATGAGAGTGG 1200
DB 1319 CAGCTGGCTTATATGAGTGTGATTAATTTGGGCTGTGAGGCTGGAGATGGAATGAGAGTGG 1378
QY 1201 TGATGAGGCAAGTATTTCTTTGAGAGAGAAATCAATTAATGAGATGGAATTTGATGATC 1260
DB 1379 TGATGAGGCAAGTATTTCTTTGAGAGAGAAATCAATTAATGAGATGGAATTTGATGATC 1438
QY 1281 CTTTACCTGATTTATTTGGCTATCTCTTCTGTTCAAGAAATTTGGGCAACAAGTGTAA 1320
DB 1439 CTTTACCTGATTTATTTGGCTATCTCTTCTGTTCAAGAAATTTGGGCAACAAGTGTAA 1498
QY 1321 TGGCAAGCTGCAAGGTTCAAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
DB 1499 TGGCAAGCTGCAAGGTTCAAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1558
QY 1381 CTGACAAATCCAAAGTATTAAGAGAGATTTAACTGTATGCCATAAAGCTCCATAAG 1440
DB 1559 CTGACAAATCCAAAGTATTAAGAGAGATTTAACTGTATGCCATAAAGCTCCATAAG 1618
QY 1441 TCACCAAGTATTTGAGGAGTATACCTTTCTTTCAAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1619 TCACCAAGTATTTGAGGAGTATACCTTTCTTTCAAGAGAGAGAGAGAGAGAGAGAGAG 1678
QY 1501 TTAAGACTTTGGGAGCTCAAGATTAATTTCCAAATCTGTCAACTCAATGATCTTAATCTC 1560
DB 1679 TTAAGACTTTGGGAGCTCAAGATTAATTTCCAAATCTGTCAACTCAATGATCTTAATCTC 1738
QY 1561 TAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
DB 1739 TAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1798
QY 1621 GTTCACTGGGCTTTGCAAGCTTTCTCATATAGTTTGTGATTAAGAAATGCCAAAGTGG 1680
DB 1799 GTTCACTGGGCTTTGCAAGCTTTCTCATATAGTTTGTGATTAAGAAATGCCAAAGTGG 1858
QY 1681 CTGCTTGATCTGAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1721
DB 1859 CTGCTTGATCTGAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1899

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RESULT 13
AAA75053
ID AAA75053 standard; cDNA, 1899 BP.
XX
AC AAA75053;
XX
DT 15-JAN-2001 (first entry)
XX
DE cDNA encoding a human heparanase polypeptide.
XX
KW Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
KW heparin-binding growth factor; cytokine; neurodegenerative plaque;
KW wound healing; infection; burn; angiogenesis; restenosis;
KW atherosclerosis; inflammation; neurodegenerative disease;
KW Gerstmann-Sträussler Syndrome; Creutzfeldt-Jakob disease; ds.
XX
OS Homo sapiens.
XX
FH Key
FH CDS
FT Location/Qualifiers
FT 94..1872
FT /*tag= a
FT /product= "heparanase"
XX
PN MO200052178-A1.

XX 08-SEP-2000.
PD
XX 14-FEB-2000; 2000MO-US003542.
PF
XX 01-MAR-1999; 99US-00258892.
PR
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.
XX
PI Pecker I, Vlodayvsky I, Feinstein E;
XX
DR MPI; 2000-579289/54.
XX P-P8DB; AAB08850.
XX
PT New polynucleotides encoding a polypeptide having heparanase activity,
PT useful in wound healing and in gene therapy, particularly in treating
PT tumor, inflammation, autoimmunity, neurodegenerative diseases.
XX
PS Claim 9; Page 121-122; 152pp; English.
XX
XX The present sequence encodes a human protein with heparanase catalytic
CC activity. The heparanase (hpa) polynucleotide is useful in gene therapy,
CC particularly in treating tumour, inflammation or autoimmunity.
CC Particularly, the polynucleotide is useful in modulating the
CC bioavailability of heparin-binding growth factors, cellular responses to
CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
CC interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular
CC susceptibility to certain viral and some bacterial and protozoa
CC infections, or disintegration of neurodegenerative plaques. The
CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or
CC radiation burns), and in the treatment of angiogenesis, restenosis,
CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
CC Strausler Syndrome or Creutzfeldt-Jakob disease), and some viral,
CC bacterial or protozoa infections
XX
SQ Sequence 1899 BP; 495 A; 433 C; 510 G; 461 T; 0 U; 0 Other;
Query Match 99.9%; Score 1719.4; DB 3; Length 1899;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTAGAGCTTTGACCTCCGCTGCGCGGAGCTGGCGGGGAGAGACAGGTGAGCCCA 60
DB 179 CTAGAGCTCTGACCTCCGCTGCGCGGAGCTGGCGGGGAGAGACAGGTGAGCCCA 238
QY 61 AGATGCTGCTGCGCTGCAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTGCTGAGGC 120
DB 239 AGATGCTGCTGCGCTGCAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTGCTGAGGC 298
QY 121 CGCTGGGTCCTCTCTCCCTGGCGGCTGCGCGCGAGCTGCGGACACAGAGCTGCTGG 180
DB 299 CGCTGGGTCCTCTCTCCCTGGCGGCTGCGCGCGAGCTGCGGACACAGAGCTGCTGG 358
QY 181 ACCTGGACTTTCTTACCCAGAGGCGGCTGCACTGTGTAGCCCCCTCTCTCTCTCTCA 240
DB 359 ACCTGGACTTTCTTACCCAGAGGCGGCTGCACTGTGTAGCCCCCTCTCTCTCTCTCA 418
QY 241 CCATTGAGCGCAACCTGGGACGAGACCGCGGTTCTCTCATCTCTGGGTTTCCAAAGC 300
DB 419 CCATTGAGCGCAACCTGGGACGAGACCGCGGTTCTCTCATCTCTGGGTTTCCAAAGC 478
QY 301 TTCTGTAACCTTGGCGCAGAGGCTTGTCTCTGCTACCTGAGGTTGTGTGGACCAAGACG 360
DB 479 TTCTGTAACCTTGGCGCAGAGGCTTGTCTCTGCTACCTGAGGTTGTGTGGACCAAGACG 538
QY 361 ACTTCTTAATTTTGCATCCCAAGAGAAATCAACTTTGAGAGAGAAATTAATGCGCAAT 420
DB 539 ACTTCTTAATTTTGCATCCCAAGAGAAATCAACTTTGAGAGAGAAATTAATGCGCAAT 598
QY 421 CTCAGTCAACCAAGATATTTGCAATATGATTCATCCCTCTGATGTGAGAGAAAGT 480

DB 599 CTCAGTCAACCAAGATATTTGCAATATGATTCATCCCTCTGATGTGAGAGAAAGT 658
QY 481 TAGGTTGGAATGGCCCTTACCCAGAGCAATTTGTAATCCCGAACAATCAACAGAAAAGT 540
DB 659 TAGGTTGGAATGGCCCTTACCCAGAGCAATTTGTAATCCCGAACAATCAACAGAAAAGT 718
QY 541 TCAAGAACAGCACTTCAAGAAAGCTCTGATATGTGCTTATACATTTTCCAAAGTCT 600
DB 719 TCAAGAACAGCACTTCAAGAAAGCTCTGATATGTGCTTATACATTTTCCAAAGTCT 778
QY 601 CAGAGCTGGAATTTTGGCTTAAATGCGTTATTAAGAACAGCAGATTTTGCAGTGA 660
DB 779 CAGAGCTGGAATTTTGGCTTAAATGCGTTATTAAGAACAGCAGATTTTGCAGTGA 838
QY 661 ACAGTTCTTAATGCTCAGTTGCTCTGAGCTATCTGCTCTTCCAAAGGGAATTAATTTCTT 720
DB 839 ACAGTTCTTAATGCTCAGTTGCTCTGAGCTATCTGCTCTTCCAAAGGGAATTAATTTCTT 898
QY 721 GGAACCTGAGCAATGAACCTTACAGTTTCTTAAGAAAGCTGATATTTTCAATGAGGT 780
DB 899 GGAACCTGAGCAATGAACCTTACAGTTTCTTAAGAAAGCTGATATTTTCAATGAGGT 958
QY 781 CGCAGTTAGAGAAATTAATTAATTCATTTGATTAACCTTGAAGAAAGTCCACTTCAAAA 840
DB 959 CGCAGTTAGAGAAATTAATTAATTCATTTGATTAACCTTGAAGAAAGTCCACTTCAAAA 1018
QY 841 ATGCAAACTTAATGCTCTGATGTTGTACGCTCCGAAGAAAGCGCTTAAGATGCTGA 900
DB 1019 ATGCAAACTTAATGCTCTGATGTTGTACGCTCCGAAGAAAGCGCTTAAGATGCTGA 1078
QY 901 AGAGCTTCTGAAGGCTGATGAGAAAGATTTGATTCAGTTACATGAGCACTACTATTT 960
DB 1079 AGAGCTTCTGAAGGCTGATGAGAAAGATTTGATTCAGTTACATGAGCACTACTATTT 1138
QY 961 TGAATGACGAGACTGCTACACAGGAGATTTTCTAAACCTTGATGATTTGACATTTTGA 1020
DB 1139 TGAATGACGAGACTGCTACACAGGAGATTTTCTAAACCTTGATGATTTGACATTTTGA 1198
QY 1021 TTTTCAATGTCGCAAAAAGTTTTCAGAGTGTGAGAGACACAGGCTTGGCAAGAGCTCT 1080
DB 1199 TTTTCAATGTCGCAAAAAGTTTTCAGAGTGTGAGAGACACAGGCTTGGCAAGAGCTCT 1258
QY 1081 GGTTAGAGAAACAAGCTCTGATATGAGAGGCGAGCGCTTGTCTATCCGACACTTTTG 1140
DB 1259 GGTTAGAGAAACAAGCTCTGATATGAGAGGCGAGCGCTTGTCTATCCGACACTTTTG 1318
QY 1141 CAGCTGGCTTTATGTGCTGATTAATTTGGGCTGTCAAGCCGAAATGGGAAATGAAGTGG 1200
DB 1319 CAGCTGGCTTTATGTGCTGATTAATTTGGGCTGTCAAGCCGAAATGGGAAATGAAGTGG 1378
QY 1201 TGAATGAGCAAGTATTTCTTTGAGACAGAAACTTACATTTTGTGATGAAAATTTCCATC 1260
DB 1379 TGAATGAGCAAGTATTTCTTTGAGACAGAAACTTACATTTTGTGATGAAAATTTCCATC 1438
QY 1261 CTTTACCGTATTTATTTGGCTATCTCTTCTGTTCAAGAAATTTGTGGGACCAAGGTTTAA 1320
DB 1439 CTTTACCGTATTTATTTGGCTATCTCTTCTGTTCAAGAAATTTGTGGGACCAAGGTTTAA 1498
QY 1321 TGGCAAGGTCGAAGTTTCAAGAGAAAGACTTGAAGTATTAATCTTATTTGCACAAA 1380
DB 1499 TGGCAAGGTCGAAGTTTCAAGAGAAAGACTTGAAGTATTAATCTTATTTGCACAAA 1558
QY 1381 CTGACATTCGAAGTATTAAGAGAAATTTAATCTGTATAGCCATAAATCTCCATAAG 1440
DB 1559 CTGACATTCGAAGTATTAAGAGAAATTTAATCTGTATAGCCATAAATCTCCATAAG 1618
QY 1441 TCACCAAGTACTTGGGTTACCTATCTTTTCTTAAACAAGTGTGATTAATACCTTC 1500
DB 1619 TCACCAAGTACTTGGGTTACCTATCTTTTCTTAAACAAGTGTGATTAATACCTTC 1678
QY 1501 TAAAGCTTTGGGACCTCATGAGATTAATTTCAAAATCTGTCAACTCAATGCTTAACTC 1560
DB 1679 TAAAGCTTTGGGACCTCATGAGATTAATTTCAAAATCTGTCAACTCAATGCTTAACTC 1738


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Db 1199 TTTCAATCTGTGCAAAAAGTTTCCAGGTGCTGAGAGCACCAGGCTGGCAAGAGTCT 1258
Qy 1081 GGTTCGAGAAACAAGCTCTGTGATATGAGAGGGGAGCCGCTTGTATCCGACACTTTG 1140
Db 1259 GGTTCGAGAAACAAGCTCTGTGATATGAGAGGGGAGCCGCTTGTATCCGACACTTTG 1318
Qy 1141 CAGTGGCTTTATGTGCTGATTAATTTGGGCTCTCAGCCCGAATGGGAATAGAATGG 1200
Db 1319 CAGTGGCTTTATGTGCTGATTAATTTGGGCTCTCAGCCCGAATGGGAATAGAATGG 1378
Qy 1201 TGATGAGCAAGATATCTTTGGAGAGAGAACTACATTTAGTGTGATGAAAATTGATC 1260
Db 1379 TGATGAGCAAGATATCTTTGGAGAGAGAACTACATTTAGTGTGATGAAAATTGATC 1438
Qy 1261 CTTTACCTGATTTATGCTATCTCTTGTTCAGAAATTTGGTGGGACCAAGGTGTTA 1320
Db 1439 CTTTACCTGATTTATGCTATCTCTTGTTCAGAAATTTGGTGGGACCAAGGTGTTA 1498
Qy 1321 TGGCAAGGCTGCAAGGTTCAAGAGAGAGAGCTTCAGATATACCTTCATTTGCAAAACA 1380
Db 1499 TGGCAAGGCTGCAAGGTTCAAGAGAGAGAGCTTCAGATATACCTTCATTTGCAAAACA 1558
Qy 1391 CTGACAAATCCAAAGGTATTAAGAAGAGATTTAACCTGTATGCCATTAACCTCCATAACG 1440
Db 1559 CTGACAAATCCAAAGGTATTAAGAAGAGATTTAACCTGTATGCCATTAACCTCCATAACG 1618
Qy 1441 TCACCAAGTACTTGGGGTTACCTCTATCCTTTTTCACAGAGAGATGATTAATACCTTC 1500
Db 1619 TCACCAAGTACTTGGGGTTACCTCTATCCTTTTTCACAGAGAGATGATTAATACCTTC 1678
Qy 1501 TAAAGCCTTTGGGAGCTGATGATTAACCTTCCAAATCTGTCCAACTCAATGGTCTAATC 1560
Db 1679 TAAAGCCTTTGGGAGCTGATGATTAACCTTCCAAATCTGTCCAACTCAATGGTCTAATC 1738
Qy 1561 TAAAGATGATGATGATCAAAACCTTGCCACCTTTATGAGAAAAACCTCTCCGGCCAGAGA 1620
Db 1739 TAAAGATGATGATGATCAAAACCTTGCCACCTTTATGAGAAAAACCTCTCCGGCCAGAGA 1798
Qy 1621 GTTCACTGGGCTTGGCAGCTTCTCATATATGTTTTTTGTATTAAGAAATGCAAAAGTTG 1680
Db 1799 GTTCACTGGGCTTGGCAGCTTCTCATATATGTTTTTTGTATTAAGAAATGCAAAAGTTG 1858
Qy 1681 CTGCTTGATCTGAATAATAATATATAGTCTGACACTG 1721
Db 1859 CTGCTTGATCTGAATAATAATATATAGTCTGACACTG 1899

RESULT 15
ADG88805
ID ADG88805 standard; cDNA; 1899 BP.
XX
AC ADG88805;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human SK-hep1 cDNA.
XX
KW Wound healing; heparanase; ulcer; burn; laceration; surgical incision;
KW necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy;
KW gene; ss.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FH CDS 94..1872
FT /*tag= a
FT /product= "Human SK-hep1 protein"
XX
XX US2003161823-A1.
XX
XX 28-AUG-2003.
XX
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PF 14-JAN-2003; 2003US-00341582.
XX
PR 31-AUG-1998; 98WO-US017954.
PR 01-MAR-1999; 99US-00258892.
PR 06-FEB-2001; 2001US-00776874.
PR 05-SEP-2001; 2001WO-1L000830.
PR 19-NOV-2001; 2001US-00988113.
XX
PA (ILAN/) ILAN N.
PA (VLAD/) VLADAVSKY I.
PA (YACO/) YACOBY-ZEEVI O.
PA (PECK/) PECKER I.
PA (FEIN/) FEINSTEIN E.
PI Ilan N, Vladavsky I, Yacoby-Zeevi O, Pecker I, Feinstein E;
XX
DR WPI: 2003-897910/82.
DR P-PSDB; ADG88804.
XX
PT Composition for treating a wound comprising recombinant heparanase is
PT useful to induce or accelerate wound healing and induce or accelerate
PT angiogenesis.
XX
PS Example 6; SEQ ID NO 15; 143bp; English.
XX
CC The present invention relates to methods and compositions for inducing
CC and/or accelerating wound healing via the catalytic activity of
CC heparanase. The invention is used to induce or accelerate a healing
CC process, particularly of an ulcer, burn, laceration, surgical incision,
CC necrosis, pressure wound, diabetic ulcer and to induce or accelerate
CC angiogenesis. The present sequence is human SK-hep1 cDNA.
XX
SQ Sequence 1899 BP; 495 A; 433 C; 510 G; 461 T; 0 U; 0 Other;
XX

Query Match 99.9%; Score 1719.4; DB 10; Length 1899;
Best local similarity 99.9%; Pred. No. 0;
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTAAGGCTTTCGACTTCCTCCGCTGCGGCGGAGCTGCGGGGAGACAGCAGTAGAGCCA 60
Db 179 CTAAGGCTTTCGACTTCCTCCGCTGCGGCGGAGCTGCGGGGAGACAGCAGTAGAGCCA 238
Qy 61 AGATGCTGCTCGCTCGAAGCTGCGCTGCGCGCGCGCTGATCTGCTGCTGCGGCG 120
Db 239 AGATGCTGCTCGCTCGAAGCTGCGCTGCGCGCGCGCTGATCTGCTGCTGCGGCG 298
Qy 121 CGTGGGCTCCCTTCTCCCTGCGGCGCTGCGCGAGCTGCGCAAGACAGAGCTGTGG 180
Db 299 CGTGGGCTCCCTTCTCCCTGCGGCGCTGCGCGAGCTGCGCAAGACAGAGCTGTGG 358
Qy 181 ACCTGAATTTCTTCAACCAAGAGCGGCTGCACTGTGTGAGAGCCCTCTGTTCCCTCA 240
Db 359 ACCTGAATTTCTTCAACCAAGAGCGGCTGCACTGTGTGAGAGCCCTCTGTTCCCTCA 418
Qy 241 CCATTGACGCCAAGCTGCGCAGAGACCGCGGTTCTCATCTCTGAGGTTCTCCAAAGC 300
Db 419 CCATTGACGCCAAGCTGCGCAGAGACCGCGGTTCTCATCTCTGAGGTTCTCCAAAGC 478
Qy 301 TTGTGACCTTGGCCAGAGGCTTGTCTCTGTGTAACCTGAGGTTTGTGTGCAACAGACG 360
Db 479 TTGTGACCTTGGCCAGAGGCTTGTCTCTGTGTAACCTGAGGTTTGTGTGCAACAGACG 538
Qy 361 ACTTCTTAATTTTGGATCCCAAGAGAAATCACTTTGAGAGAAATTAATGCGCAAT 420
Db 539 ACTTCTTAATTTTGGATCCCAAGAGAAATCACTTTGAGAGAAATTAATGCGCAAT 598
Qy 421 CTCAGTCAACCAAGATATTTGCAATATAGATCATCTCTGATGTGAGAGAAAGT 480
Db 599 CTCAGTCAACCAAGATATTTGCAATATAGATCATCTCTGATGTGAGAGAAAGT 658
Qy 481 TAGGTTGGAATGGCCCTTACCAAGAGCAATTTGTAATTCAGAAACATCAACCAAAAGT 540
Db 659 TAGGTTGGAATGGCCCTTACCAAGAGCAATTTGTAATTCAGAAACATCAACCAAAAGT 718
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